

P03371US0 Sequence listing).txt  
SEQUENCE LISTING

<110> F2G LIMITED  
<120> 2031 OXIDOREDUCTASE  
<130> HO-P03371US0  
<140> PCT/GB05/000623  
<141> 2005-02-18  
<150> GB 0403746.1  
<151> 2004-02-19  
<150> GB 0424080.0  
<151> 2004-10-29  
<160> 101  
<170> PatentIn version 3.2  
<210> 1  
<211> 1908  
<212> DNA  
<213> Aspergillus fumigatus

<400> 1  
gttcgacgtc attgccacgt ttcgacccaa gggcagacgc catgtcgccg agcgatcgcc 60  
gcgatatgcc tcgaatttgc gccattcggc atccagtttc cagtgccctt ccccgaatga 120  
ctgtctccac tattcggcaa gattgtaaat caagcctgaa gaagcggagc aattcttgga 180  
agtcgtatgt tctactgatt tctgtgcctg gcgcagacgg gtatataaat aaagatcacc 240  
gcaccgagga gtttcttacc aacccatcaa taaccatcca caatctccta caacaaaaat 300  
gactgtcgcc gatatcgacg ttctctcctgc cgagggcatc ccctacttca ctccggccca 360  
gaaccctcct gccggtacgg cagctaacct ccagaccaat ggccagaaga tccccaagct 420  
cttcacgccc ttgaccatcc gtggcgctcac cttccagaac cgccttggtg taagtccgtt 480  
tgcccttgct catatcgacg aaagctaata ccccgtcagc tcgcgcccct ctgccaatac 540  
tccgcccagg acggccacat gaccgactac cacatcgccc atctgggtgg gatcgcccaa 600  
cgcggaacct gcctgatgct gattgaggcg accgccgtcc agcccgaagg ccgcatcacc 660  
cctcaggatg tcggtctgtg gaaggactcc cagatcgccc cgatgcgccg ggtcatcgac 720  
ttcgtgcaca gccagggcca gaagatcggc gtgcagcttg cccatgccgg ccggaaagcc 780  
accaccgttg cgccctggat ctcatctctg gccatcgca cggagaaggt cggcggatgg 840  
ccggaccgcy tcaaagggcc cggcgatatc ccctttgcgg agcccttcgc caagcccaag 900  
gccatgacgc tggatgagat cgagcagttc aagaaggact ggggtggcggc cacgaagcgc 960  
gccatcgccg ccggtgcgga ctttgtcgag attcacaatg cgcattggata cctgctgtcg 1020  
tcattcctct cgccggccgc caacaaccgc acggaccagt acggcggggc gttcgagaac 1080

P03371US0 Sequence listing).txt

cgcatccggc tgtctctcga gattgcgag ttgactcggg acgccgtcgg ccctcatgtg	1140
cccgttttcc tgcgcatttc ggcctcggac tgggtgcgagg agaccctgcc ggagcagagc	1200
tggaagtcgg aggataccgt gcggttcgag caggagctgg tcaagcaggg cgccgttgat	1260
ctgatcgata tcagcagcgg tgggtgttctc gcgcagcaga agatcaagtc cggccctgcc	1320
ttccaggtgc cttttgccgt ggccgtgaag aaggccgtcg gcgacaagct gctggttgcc	1380
gccgtgggtg ccatcaccaa cggcaagcag gcgaatcaga ttctagagga gcaggatatc	1440
gacgttgcg c tgggttgccg tgggttccag aaggatccc gtctggcctg gacgtttgct	1500
cagcacctcg gcgtcgaaat ctccatggcc aaccagatcc gctggggctt caccggcgt	1560
ggaggcacc cgtacattga tccttcggtg tacaagcagt ctattttcga tgtatagagt	1620
atagatagag ttgaagatga tacctcatag acgatcaatg gacccttgca tattatttct	1680
cgtctcctgc gtatgttcaa ggtattcaca gtagctgcgt cctcttaagt ttctccgtca	1740
ttcgttctat tctactcaa tcgcaacgca tggcgaccac ggatcgagtc gaatttctcc	1800
gtcgttcgta tctgatcaat ataaaaagcg gggaatggct tgaccccgcg cagaatgtcg	1860
atctcttcgc aaactctcgg tgtataggac gctcagcaac gatcaagg	1908

<210> 2

<211> 1445

<212> DNA

<213> *Aspergillus fumigatus*

<400> 2

gtatgttcta ctgatttctg tgcctggcgc agacgggtat ataaataaag atcaccgcac	60
cgaggagttt cttaccaacc catcaataac catccacaat ctctacaac aaaaatgact	120
gtcgccgata tcgacgttcc tcctgccgag ggcattcccct acttcactcc ggcccagaac	180
cctcctgccc gtacggcagc taacccccag accaatggcc agaagatccc caagctcttc	240
acgcccttga ccatccgtgg cgtcaccttc cagaaccgcc ttggtctcgc gcccctctgc	300
caataactccg cccaggacgg ccacatgacc gactaccaca tcgcccattt ggggtgggac	360
gcccacgcg gacccggcct gatgctgatt gaggcgaccg ccgtccagcc cgaaggccgc	420
atcacccctc aggatgtcgg tctgtggaag gactcccaga tcgccccgat gcgccgggtc	480
atcgacttcg tgcacagcca gggccagaag atcggcgtgc agcttgcca tgccggccgg	540
aaagccacca ccgttgcgcc ctggatctca ttctcggcc tgcgcagga gaaggtcggc	600
ggatggccgg acccggtca aagggccgg cgatatcccc ttgcgaggc ccttcgcaa	660
gcccaggcc atgacgtgg atgagatcga gcagttcaag aaggactggg tggcgccac	720
gaagcgcgcc atcgccgcc gtgaggactt tgctgagatt cacaatgcgc atggatacct	780
gctgtcgtca ttctctcgc cggccgcaa caaccgcag gaccagtacg gcgggtcgtt	840

P03371US0 Sequence listing).txt

```

cgagaaccgc atccggctgt ctctcgagat tgcgcagttg actcgggacg ccgtcggccc 900
tcatgtgccc gttttcctgc gcatttcggc ctcggactgg tgcgaggaga ccctgccgga 960
gcagagctgg aagtcggagg ataccgtgcg gttcgcgcag gagctggtca agcagggcgc 1020
cgttgatctg atcgatatca gcagcgggtgg tgttctcgcg cagcagaaga tcaagtccgg 1080
ccctgccttc caggtgcctt ttgccgtggc cgtgaagaag gccgtcggcg acaagctgct 1140
ggttgccgcc gtgggtgccca tcaccaacgg caagcaggcg aatcagattc tagaggagca 1200
ggatatcgac gttgcgctgg ttggccgtgg gttccagaag gatcccggtc tggcctggac 1260
gtttgctcag cacctcggcg tcgaaatctc catggccaac cagatccgct ggggcttcac 1320
ccggcgtgga ggcaccccg t acattgatcc ttcggtgtac aagcagtcta ttttcgatgt 1380
atagagtata gatagagttg aagatgatac ctcatagacg atcaatggac ctttgcatat 1440
tattt 1445

```

```

<210> 3
<211> 422
<212> PRT
<213> Aspergillus fumigatus
<400> 3

```

Met Thr Val Ala Asp Ile Asp Val Pro Pro Ala Glu Gly Ile Pro Tyr  
1 5 10 15

Phe Thr Pro Ala Gln Asn Pro Pro Ala Gly Thr Ala Ala Asn Pro Gln  
20 25 30

Thr Asn Gly Gln Lys Ile Pro Lys Leu Phe Thr Pro Leu Thr Ile Arg  
35 40 45

Gly Val Thr Phe Gln Asn Arg Leu Gly Leu Ala Pro Leu Cys Gln Tyr  
50 55 60

Ser Ala Gln Asp Gly His Met Thr Asp Tyr His Ile Ala His Leu Gly  
65 70 75 80

Gly Ile Ala Gln Arg Gly Pro Gly Leu Met Leu Ile Glu Ala Thr Ala  
85 90 95

Val Gln Pro Glu Gly Arg Ile Thr Pro Gln Asp Val Gly Leu Trp Lys  
100 105 110

Asp Ser Gln Ile Ala Pro Met Arg Arg Val Ile Asp Phe Val His Ser  
115 120 125

Gln Gly Gln Lys Ile Gly Val Gln Leu Ala His Ala Gly Arg Lys Ala  
Page 3

P03371US0 Sequence listing).txt

130

135

140

Thr Thr Val Ala Pro Trp Ile Ser Phe Ser Ala Ile Ala Thr Glu Lys  
145 150 155 160

Val Gly Gly Trp Pro Asp Arg Val Lys Gly Pro Gly Asp Ile Pro Phe  
165 170 175

Ala Glu Pro Phe Ala Lys Pro Lys Ala Met Thr Leu Asp Glu Ile Glu  
180 185 190

Gln Phe Lys Lys Asp Trp Val Ala Ala Thr Lys Arg Ala Ile Ala Ala  
195 200 205

Gly Ala Asp Phe Val Glu Ile His Asn Ala His Gly Tyr Leu Leu Ser  
210 215 220

Ser Phe Leu Ser Pro Ala Ala Asn Asn Arg Thr Asp Gln Tyr Gly Gly  
225 230 235 240

Ser Phe Glu Asn Arg Ile Arg Leu Ser Leu Glu Ile Ala Gln Leu Thr  
245 250 255

Arg Asp Ala Val Gly Pro His Val Pro Val Phe Leu Arg Ile Ser Ala  
260 265 270

Ser Asp Trp Cys Glu Glu Thr Leu Pro Glu Gln Ser Trp Lys Ser Glu  
275 280 285

Asp Thr Val Arg Phe Ala Gln Glu Leu Val Lys Gln Gly Ala Val Asp  
290 295 300

Leu Ile Asp Ile Ser Ser Gly Gly Val Leu Ala Gln Gln Lys Ile Lys  
305 310 315 320

Ser Gly Pro Ala Phe Gln Val Pro Phe Ala Val Ala Val Lys Lys Ala  
325 330 335

Val Gly Asp Lys Leu Leu Val Ala Ala Val Gly Ala Ile Thr Asn Gly  
340 345 350

Lys Gln Ala Asn Gln Ile Leu Glu Glu Gln Asp Ile Asp Val Ala Leu  
355 360 365

Val Gly Arg Gly Phe Gln Lys Asp Pro Gly Leu Ala Trp Thr Phe Ala  
370 375 380

P03371US0 Sequence listing).txt

Gln His Leu Gly Val Glu Ile Ser Met Ala Asn Gln Ile Arg Trp Gly  
385 390 395 400

Phe Thr Arg Arg Gly Gly Thr Pro Tyr Ile Asp Pro Ser Val Tyr Lys  
405 410 415

Gln Ser Ile Phe Asp Val  
420

<210> 4  
<211> 1352  
<212> DNA  
<213> Aspergillus fumigatus

<400> 4  
atgtcgcaac ctgttgtgcc tgacatcgag aacaaacccg cgccgggtat ctcgtacttt 60  
actccggcgc aagagccgcc tgctggcacc gctgctaadc ctcagtctga tggatcggca 120  
cctcccaagc tcttcgggcc gctttcggtg cgggggtctga cttttcacia tcgcattggc 180  
gtgagtgcag tccaggcaat tatgctatcc atcctatgcg agcccttgca ttggaacagc 240  
cgcttacagg gaatgataat gagtagctat cgccactctg ccaataactca gccgacgatg 300  
gacacatgac tccctggcat atggcacatc ttggagggat tgcccagcga gggccaggat 360  
tcttgatggt cgaggcaaca gcagtcgaac cggaaggcag gatcaccctg caggacctgg 420  
gactatggaa agactcgcag attgagccat tgagccgcgt gatcgagttt gtccacagtc 480  
agaaccagct tatcggcgtg cagatcgcac acgcaggctg caaggccagc accgtcgcgc 540  
catggctctc ggccaacgat accgcctccg agaagatggg cggttgcca ggccgcgtca 600  
aaggcccgac aaatgtgccc ttcaccgtta agaaccctgt gccgaaggag atgaccaagc 660  
aggatatcga ggatctgaag accgcctggg tggccgctgt caaacgggct gttaaggccg 720  
gagccgactt tatcgagatc cacaatgcgc atggctatct tctgatgtcg ttcctctccc 780  
ctgcggtcaa cagagaaca gacgagtacg gaggcagttt tgagaatcgc atccgggtca 840  
gtctggagat cgccaagctc acccgcgaaa atgtgcccga ggatatgcct gtcttcctgc 900  
gggtctccgc caccgattgg ctggaggagg tgcagccgaa caagcccagc tggcgaggcg 960  
tggacactgt ccgatttgcg aagatcctgg cagaaacggg ttacgttgac gtgcttgacg 1020  
tgagcagtgg cggcactcat tcggagcagc atatccacgc gaagccaggc ttccaggcac 1080  
cctttgctat tgccgtcaag aacgccgtcg gggacaaact cgcagtggca tcagtgggta 1140  
tgattgccag cgcgcatttg gccaatcctt tgttgagaaa ggacggactg gaccttgatg 1200  
tggttggacg tggcttcagc aagaacccgg ggctgggtgt ggctggggcc gacgagctga 1260  
atgtagagat ctccatggct aatcagatcc gatgggggtt ctcgcggcgc ggtgctggtc 1320  
cttacctcag gaagaaactc gagaagatat aa 1352

P03371US0 Sequence listing).txt

<210> 5  
 <211> 1266  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 5  
 atgtcgcgaac ctgtttgtgcc tgacatcgag aacaaacccg cgccgggtat ctcgtacttt 60  
 actccggcgc aagagccgcc tgctggcacc gctgctaata ctcagtctga tggatcggca 120  
 cctcccaagc tcttccggcc gctttcgggtg cggggctctga cctttcacia tcgcattggc 180  
 ctatcgccac tctgccaata ctcagccgac gatggacaca tgactccctg gcatatggca 240  
 catcttggag ggattgcccc gcgagggcca ggattcttga tggtcgaggc aacagcagtc 300  
 gaaccggaag gcaggatcac cccgcaggac ctgggactat ggaaagactc gcagattgag 360  
 ccattgagcc gcgtgatcga gtttgtccac agtcagaacc agcttatcgg cgtgcagatc 420  
 gcacacgcag gtcgcaaggc cagcaccgtc gcgccatggc tctcggccaa cgataccgcc 480  
 tccgagaaga tgggctggctg gccaggccgc gtcaaaggcc cgacaaatgt gcccttcacc 540  
 gttaagaacc ctgtgccgaa ggagatgacc aagcaggata tcgaggatct gaagaccgcc 600  
 tgggtggccg ctgtcaaacg ggctgttaag gccggagccg actttatcga gatccacaat 660  
 gcgcattggc atcttctgat gtcgttcctc tcccctgcgg tcaacacgag aacagacgag 720  
 tacggaggca gttttgagaa tcgcatccgg ctcagtctgg agatcgccaa gctcaccgcg 780  
 gaaaatgtgc ccaaggatat gcctgtcttc ctgcgggtct ccgccaccga ttggctggag 840  
 gaggtgcagc cgaacaagcc cagctggcga ggcgtggaca ctgtccgatt tgcgaagatc 900  
 ctggcagaaa cgggttacgt tgacgtgctt gacgtgagca gtggcggcac tcattcggag 960  
 cagcatatcc acgcgaagcc aggttccag gcaccctttg ctattgccgt caagaacgcc 1020  
 gtcggggaca aactcgcagt ggcattcagt ggtatgattg ccagcgcgca tttggccaat 1080  
 tccttggttg agaaggacgg actggacctt gtgctggttg gacgtggctt ccagaagaac 1140  
 ccggggctgg tgtgggcgtg ggccgacgag ctgaatgtag agatctccat ggctaatacag 1200  
 atccgatggg gtttctcgcg gcgcggtgct ggtccttacc tcaggaagaa actcgagaag 1260  
 atataa 1266

<210> 6  
 <211> 421  
 <212> PRT  
 <213> *Aspergillus fumigatus*

<400> 6

Met Ser Gln Pro Val Val Pro Asp Ile Glu Asn Lys Pro Ala Pro Gly  
 1 5 10 15

P03371US0 Sequence listing).txt

Ile Ser Tyr Phe Thr Pro Ala Gln Glu Pro Pro Ala Gly Thr Ala Ala  
20 25 30

Asn Pro Gln Ser Asp Gly Ser Ala Pro Pro Lys Leu Phe Arg Pro Leu  
35 40 45

Ser Val Arg Gly Leu Thr Phe His Asn Arg Ile Gly Leu Ser Pro Leu  
50 55 60

Cys Gln Tyr Ser Ala Asp Asp Gly His Met Thr Pro Trp His Met Ala  
65 70 75 80

His Leu Gly Gly Ile Ala Gln Arg Gly Pro Gly Phe Leu Met Val Glu  
85 90 95

Ala Thr Ala Val Glu Pro Glu Gly Arg Ile Thr Pro Gln Asp Leu Gly  
100 105 110

Leu Trp Lys Asp Ser Gln Ile Glu Pro Leu Ser Arg Val Ile Glu Phe  
115 120 125

Val His Ser Gln Asn Gln Leu Ile Gly Val Gln Ile Ala His Ala Gly  
130 135 140

Arg Lys Ala Ser Thr Val Ala Pro Trp Leu Ser Ala Asn Asp Thr Ala  
145 150 155 160

Ser Glu Lys Met Gly Gly Trp Pro Gly Arg Val Lys Gly Pro Thr Asn  
165 170 175

Val Pro Phe Thr Val Lys Asn Pro Val Pro Lys Glu Met Thr Lys Gln  
180 185 190

Asp Ile Glu Asp Leu Lys Thr Ala Trp Val Ala Ala Val Lys Arg Ala  
195 200 205

Val Lys Ala Gly Ala Asp Phe Ile Glu Ile His Asn Ala His Gly Tyr  
210 215 220

Leu Leu Met Ser Phe Leu Ser Pro Ala Val Asn Thr Arg Thr Asp Glu  
225 230 235 240

Tyr Gly Gly Ser Phe Glu Asn Arg Ile Arg Leu Ser Leu Glu Ile Ala  
245 250 255

Lys Leu Thr Arg Glu Asn Val Pro Lys Asp Met Pro Val Phe Leu Arg  
260 265 270

P03371US0 Sequence listing).txt

Val Ser Ala Thr Asp Trp Leu Glu Glu Val Gln Pro Asn Lys Pro Ser  
275 280 285

Trp Arg Gly Val Asp Thr Val Arg Phe Ala Lys Ile Leu Ala Glu Thr  
290 295 300

Gly Tyr Val Asp Val Leu Asp Val Ser Ser Gly Gly Thr His Ser Glu  
305 310 315 320

Gln His Ile His Ala Lys Pro Gly Phe Gln Ala Pro Phe Ala Ile Ala  
325 330 335

Val Lys Asn Ala Val Gly Asp Lys Leu Ala Val Ala Ser Val Gly Met  
340 345 350

Ile Ala Ser Ala His Leu Ala Asn Ser Leu Leu Glu Lys Asp Gly Leu  
355 360 365

Asp Leu Val Leu Val Gly Arg Gly Phe Gln Lys Asn Pro Gly Leu Val  
370 375 380

Trp Ala Trp Ala Asp Glu Leu Asn Val Glu Ile Ser Met Ala Asn Gln  
385 390 395 400

Ile Arg Trp Gly Phe Ser Arg Arg Gly Ala Gly Pro Tyr Leu Arg Lys  
405 410 415

Lys Leu Glu Lys Ile  
420

<210> 7  
<211> 1329  
<212> DNA  
<213> Aspergillus fumigatus

<400> 7  
atgggttcca acgccttccg gtccccgcc gtcaccaagt cctcctccac cccctactac 60  
actcccgcc acaatggagg cgccgccctg caccgacg accccacgac ccctacgctc 120  
ttccggccct tacaaatccg caatgtgacg ctcaagaacc gcatcatggt gtcgcccattg 180  
tgcatgtact cctgcgagtc ggaccgctg tctccccacg tcggcgccct aacaaactac 240  
cacctggcgc atctgggcca cctcgccctc aaaggcgag gcctcgtctt catcgaagcc 300  
accgcccgtg agcccaacgg gcgcatctcc cccaacgact cgggcctctg gcaggacggc 360  
accacctcgg aacaattcct ggggctgaag cgggtcgtcg agttcatgca cgcacagggc 420  
gccaaggctg ggatccagct tgcgcatgcg ggccggaaag cgagtgccgt tgcgcccgtg 480

P03371US0 Sequence listing).txt

```

ctggcggcgc aggcgggcaa gtcgagtctg aaggcggatg agagcgttgg cgggtggccc 540
gcggatgttg tgggtccgtc gggcggggag gagcatatct ttagtcccga ggaggatgcg 600
tattgggtgc cgcgggcgtc gagcacggcc gaggtccgtc aggtggtggc ggcgtttgcg 660
aagagcgcgc ggctagcggg gcaggctggg gtggatgtta tcgagatcca tggggcgcgcat 720
ggctatctca tcaacgagtt cctgagcccc gtcacgaata agcggacgga tgcgtacggc 780
gggagctttg agaaccggac ccggatcgtg cgcgaggttg cggcggctat tcgtgcggtg 840
attcccaggg ggatgcccct gtttctgcgt atcagcgcca cggagtgggt ggagggtcag 900
ccggtggccg cggagtcggg cagctgggat atgcagagct cgctggagct ggtcaagaag 960
ctgcccgaat ggggcattga cctggtggat gtcagctccg ccgcgaacca caaggaccag 1020
aagatcaacc tgcacacggc ctaccagacg gacctggccg ggcagattcg ccaggccatc 1080
cgagcggctg gcgcgtcgac tcttgtgggt gctgtaggtc tgatcaccga ttcggaacag 1140
gcgagggggac tagttcaggg agcggacgag gcgactgcag ccgaggcaat gctgtcggga 1200
cctgaacca aggcggatgc cattctgata gcccgtcagt tcctgcgcga gccagaatgg 1260
gtgttttcca cggcgagaaa gttgggcgtg ccggtgactg tcccggtgca gtttggcagg 1320
gccatttag 1329

```

```

<210> 8
<211> 442
<212> PRT
<213> Aspergillus fumigatus

```

<400> 8

```

Met Gly Ser Asn Ala Phe Arg Ser Pro Ala Val Thr Lys Ser Ser Ser
1          5          10          15

```

```

Thr Pro Tyr Tyr Thr Pro Ala Asn Asn Gly Gly Ala Ala Leu His Pro
20          25          30

```

```

Asp Asp Pro Thr Thr Pro Thr Leu Phe Arg Pro Leu Gln Ile Arg Asn
35          40          45

```

```

Val Thr Leu Lys Asn Arg Ile Met Val Ser Pro Met Cys Met Tyr Ser
50          55          60

```

```

Cys Glu Ser Asp Pro Ser Ser Pro His Val Gly Ala Leu Thr Asn Tyr
65          70          75          80

```

```

His Leu Ala His Leu Gly His Leu Ala Leu Lys Gly Ala Gly Leu Val
85          90          95

```

P03371US0 Sequence listing).txt

Phe Ile Glu Ala Thr Ala Val Gln Pro Asn Gly Arg Ile Ser Pro Asn  
100 105 110

Asp Ser Gly Leu Trp Gln Asp Gly Thr Thr Ser Glu Gln Phe Leu Gly  
115 120 125

Leu Lys Arg Val Val Glu Phe Met His Ala Gln Gly Ala Lys Val Gly  
130 135 140

Ile Gln Leu Ala His Ala Gly Arg Lys Ala Ser Ala Val Ala Pro Trp  
145 150 155 160

Leu Ala Ala Gln Ala Gly Lys Ser Ser Leu Lys Ala Asp Glu Ser Val  
165 170 175

Gly Gly Trp Pro Ala Asp Val Val Gly Pro Ser Gly Gly Glu Glu His  
180 185 190

Ile Phe Ser Pro Glu Glu Asp Ala Tyr Trp Val Pro Arg Ala Leu Ser  
195 200 205

Thr Ala Glu Val Arg Gln Val Val Ala Ala Phe Ala Lys Ser Ala Arg  
210 215 220

Leu Ala Val Gln Ala Gly Val Asp Val Ile Glu Ile His Gly Ala His  
225 230 235 240

Gly Tyr Leu Ile Asn Glu Phe Leu Ser Pro Val Thr Asn Lys Arg Thr  
245 250 255

Asp Ala Tyr Gly Gly Ser Phe Glu Asn Arg Thr Arg Ile Val Arg Glu  
260 265 270

Val Ala Ala Ala Ile Arg Ala Val Ile Pro Glu Gly Met Pro Leu Phe  
275 280 285

Leu Arg Ile Ser Ala Thr Glu Trp Leu Glu Gly Gln Pro Val Ala Ala  
290 295 300

Glu Ser Gly Ser Trp Asp Met Gln Ser Ser Leu Glu Leu Val Lys Lys  
305 310 315 320

Leu Pro Glu Trp Gly Ile Asp Leu Val Asp Val Ser Ser Ala Ala Asn  
325 330 335

His Lys Asp Gln Lys Ile Asn Leu His Thr Ala Tyr Gln Thr Asp Leu  
340 345 350

P03371US0 Sequence listing).txt

Ala Gly Gln Ile Arg Gln Ala Ile Arg Ala Ala Gly Ala Ser Thr Leu  
355 360 365

Val Gly Ala Val Gly Leu Ile Thr Asp Ser Glu Gln Ala Arg Gly Leu  
370 375 380

Val Gln Gly Ala Asp Glu Ala Thr Ala Ala Glu Ala Met Leu Ser Gly  
385 390 395 400

Pro Glu Pro Lys Ala Asp Ala Ile Leu Ile Ala Arg Gln Phe Leu Arg  
405 410 415

Glu Pro Glu Trp Val Phe Ser Thr Ala Arg Lys Leu Gly Val Pro Val  
420 425 430

Thr Val Pro Val Gln Phe Gly Arg Ala Ile  
435 440

<210> 9  
<211> 1269  
<212> DNA  
<213> Aspergillus nidulans

<400> 9  
atggctctcc ctgacgtcga aaacaccccc gccgccggca tcccctactt tacaccagca 60  
cagaaccctc ctgctggaac agctgccaac ccgcaaacca gcggcaatgc cgtccccaag 120  
ctgtacacac ctctgacggt gcgtgggggtg accttcaca acagacttgg cctcgcgccg 180  
ctctgccagt actccgcaga agacggccac atgacagact accacatcgc gcacttggga 240  
gggtattgcc agcgcggccc cgggtctcatg atgatcgagg caacctcgt ctcacctgaa 300  
ggcagaatca cgccgcagga cgtcggttta tggaaggact cgcagattgc gcccatgaag 360  
cgcgatcatg acttcgtgca ctcgcagtcc cagaagattg gcgtgcagat tgcccacgcc 420  
ggccgcaagg cttcgaacat cggcccttgg ctcatgaaca agggcatcgt cgcgacggag 480  
aaggtcggtg gctggccgga tcgtgtgatc ggcccgtcca ccgtgccctt ccacgagact 540  
ttccccaccc ccaaggccat gaccaaggac gacatcgagc agttcaagcg cgactggttt 600  
gatgcgtgca agcgggcat tgccgctggc gcggacttca tcgagatcca caatgccac 660  
gggtatcttc tctcgtcttt cctatcaccg tcttccaaca cgcgaccga cgagtacggc 720  
ggctcctttg agaaccgcat ccggctctct ctcgaaatcg ccaggtcac ccgtgacgcc 780  
gtcggcccca acgttctgt ttttctccgt gtctccgcga cggactggat cgaggagacc 840  
ctccccgagg aatcgtggaa gctctctgac tccgtccgct tcgccgaagc cctcgctgcc 900  
cagggcgcta ttgacctgat cgacgtctct tccggcgggtg tccacgccgc gcagaagatc 960

P03371US0 Sequence listing).txt

aagtccgggc cggctttcca ggctcccttc gctgtggcta tcaagaaggc cgttggcgat 1020  
 aagctccttg ttgcgacggt gggcacgata acgaacggta agcaggcgaa caagctgctt 1080  
 gaggaggagg gattggatgt tgcgcttggt ggacgtgggt tccagaagga tcccgggtctg 1140  
 gcgtggactt tcgcgcagca tcttgatgtt gagattgcga tggcgagtca gattcgggtgg 1200  
 ggattcaciaa ggcgcggggg cacgccttat atcgacccca aagcttataa ggagagcatc 1260  
 tttgagtaa 1269

<210> 10  
 <211> 422  
 <212> PRT  
 <213> Aspergillus nidulans

<400> 10

Met Ala Leu Pro Asp Val Glu Asn Thr Pro Ala Ala Gly Ile Pro Tyr  
 1 5 10 15

Phe Thr Pro Ala Gln Asn Pro Pro Ala Gly Thr Ala Ala Asn Pro Gln  
 20 25 30

Thr Ser Gly Asn Ala Val Pro Lys Leu Tyr Thr Pro Leu Thr Val Arg  
 35 40 45

Gly Val Thr Phe His Asn Arg Leu Gly Leu Ala Pro Leu Cys Gln Tyr  
 50 55 60

Ser Ala Glu Asp Gly His Met Thr Asp Tyr His Ile Ala His Leu Gly  
 65 70 75 80

Gly Ile Ala Gln Arg Gly Pro Gly Leu Met Met Ile Glu Ala Thr Ser  
 85 90 95

Val Ser Pro Glu Gly Arg Ile Thr Pro Gln Asp Val Gly Leu Trp Lys  
 100 105 110

Asp Ser Gln Ile Ala Pro Met Lys Arg Val Ile Asp Phe Val His Ser  
 115 120 125

Gln Ser Gln Lys Ile Gly Val Gln Ile Ala His Ala Gly Arg Lys Ala  
 130 135 140

Ser Asn Ile Ala Pro Trp Leu Met Asn Lys Gly Ile Val Ala Thr Glu  
 145 150 155 160

Lys Val Gly Gly Trp Pro Asp Arg Val Ile Gly Pro Ser Thr Val Pro  
 165 170 175

P03371US0 Sequence listing).txt

Phe His Glu Thr Phe Pro Thr Pro Lys Ala Met Thr Lys Asp Asp Ile  
 180 185 190  
 Glu Gln Phe Lys Arg Asp Trp Phe Asp Ala Cys Lys Arg Ala Ile Ala  
 195 200 205  
 Ala Gly Ala Asp Phe Ile Glu Ile His Asn Ala His Gly Tyr Leu Leu  
 210 215 220  
 Ser Ser Phe Leu Ser Pro Ser Ser Asn Thr Arg Thr Asp Glu Tyr Gly  
 225 230 235 240  
 Gly Ser Phe Glu Asn Arg Ile Arg Leu Ser Leu Glu Ile Ala Gln Val  
 245 250 255  
 Thr Arg Asp Ala Val Gly Pro Asn Val Pro Val Phe Leu Arg Val Ser  
 260 265 270  
 Ala Thr Asp Trp Ile Glu Glu Thr Leu Pro Glu Glu Ser Trp Lys Leu  
 275 280 285  
 Ser Asp Ser Val Arg Phe Ala Glu Ala Leu Ala Ala Gln Gly Ala Ile  
 290 295 300  
 Asp Leu Ile Asp Val Ser Ser Gly Gly Val His Ala Ala Gln Lys Ile  
 305 310 315 320  
 Lys Ser Gly Pro Ala Phe Gln Ala Pro Phe Ala Val Ala Ile Lys Lys  
 325 330 335  
 Ala Val Gly Asp Lys Leu Leu Val Ala Thr Val Gly Thr Ile Thr Asn  
 340 345 350  
 Gly Lys Gln Ala Asn Lys Leu Leu Glu Glu Glu Gly Leu Asp Val Ala  
 355 360 365  
 Leu Val Gly Arg Gly Phe Gln Lys Asp Pro Gly Leu Ala Trp Thr Phe  
 370 375 380  
 Ala Gln His Leu Asp Val Glu Ile Ala Met Ala Ser Gln Ile Arg Trp  
 385 390 395 400  
 Gly Phe Thr Arg Arg Gly Gly Thr Pro Tyr Ile Asp Pro Lys Ala Tyr  
 405 410 415  
 Lys Glu Ser Ile Phe Glu  
 420

P03371US0 Sequence listing).txt

<210> 11  
 <211> 1299  
 <212> DNA  
 <213> Candida albicans

<400> 11  
 atgacagttc cataccaagt aaaaccatca gatgaaatca aagggtgctcc tgaggtttcc 60  
 tattacactc cagaacagcc tgttcgggct ggtacttttt atccccaatc gtcagatgaa 120  
 gttgctccca aaatTTTTca accttttaaag attggtaagc ttgctttgcc aaacagaatt 180  
 ggggtatctc caatgtgtca atattctgct gattataatt ttgaagcaac tccataccat 240  
 ttaatccatt atggttcatt agtgaatcgt gggccaggta tcaccattgt tgaaagcacg 300  
 gctgtttctc ctgaggggtg attatcacct catgatttag gaatctggaa ggatgaacaa 360  
 gcagagaaat tgaaaccaat tgtcgattac gctcattctc aaaagcaatt aattgccatc 420  
 caattgggcc atggtggtag aaaagcttct ggtcagccct tatttttgca cttggaacaa 480  
 gttgcagata aatctgtcaa tgggtttgcc gacaaagcag ttgctccttc tgcattggca 540  
 ttcagaccaa atggtaattt acctgttcct aatgagttga ccaaagatga aatcaaacgt 600  
 gttgttaagg attttggtgc tgctgctaga agagctgttg aaatcagtgg ctttgatgca 660  
 gttgagattc atggtgctca tggttatttg attaatgagt tctatagtcc tatttcaaac 720  
 aagagaacag atgaatacgg tggcagtttt gaaaatagaa ccagattttt aaaggaagtt 780  
 atcgatagtg ttaaatacag tattccaaac gatgtttccag tgtttttgag aatctctgct 840  
 gctgaaaata gtcctgatcc agaagcttgg actattgaag attccaaaaa attagctgac 900  
 attttagtag aaaaggggat tgctttgggt gatgtttcat ctggtggtaa cgattataga 960  
 caaccaccaa gatctgggat cagtaaagag ttgagagagc caatccatgt tccgttgtct 1020  
 cgtgcaatta aacaacatgt tggtgacaag ttattgggtca gttgcgttgg tgggcttgaa 1080  
 aaagatcctg aattgctcaa caaatattta gaagaaggaa catttgatct tgctttgatc 1140  
 ggtagaggat ttttaagaaa tccaggtttg gtatgggagt ttgccgataa acttggtggt 1200  
 agactccacc aggccttgca gttaggttgg ggtttctggc ccaacaaaca acaaattggt 1260  
 gatttgattg aaagaacatc taaattagaa gtaaattag 1299

<210> 12  
 <211> 432  
 <212> PRT  
 <213> Candida albicans

<400> 12

Met Thr Val Pro Tyr Gln Val Lys Pro Ser Asp Glu Ile Lys Gly Ala  
 1 5 10 15

P03371US0 Sequence listing).txt

Pro Glu Val Ser Tyr Tyr Thr Pro Glu Gln Pro Val Pro Ala Gly Thr  
20 25 30

Phe Tyr Pro Gln Ser Ser Asp Glu Val Ala Pro Lys Ile Phe Gln Pro  
35 40 45

Leu Lys Ile Gly Lys Leu Ala Leu Pro Asn Arg Ile Gly Val Ser Pro  
50 55 60

Met Cys Gln Tyr Ser Ala Asp Tyr Asn Phe Glu Ala Thr Pro Tyr His  
65 70 75 80

Leu Ile His Tyr Gly Ser Leu Val Asn Arg Gly Pro Gly Ile Thr Ile  
85 90 95

Val Glu Ser Thr Ala Val Ser Pro Glu Gly Gly Leu Ser Pro His Asp  
100 105 110

Leu Gly Ile Trp Lys Asp Glu Gln Ala Glu Lys Leu Lys Pro Ile Val  
115 120 125

Asp Tyr Ala His Ser Gln Lys Gln Leu Ile Ala Ile Gln Leu Gly His  
130 135 140

Gly Gly Arg Lys Ala Ser Gly Gln Pro Leu Phe Leu His Leu Glu Gln  
145 150 155 160

Val Ala Asp Lys Ser Val Asn Gly Phe Ala Asp Lys Ala Val Ala Pro  
165 170 175

Ser Ala Leu Ala Phe Arg Pro Asn Gly Asn Leu Pro Val Pro Asn Glu  
180 185 190

Leu Thr Lys Asp Glu Ile Lys Arg Val Val Lys Asp Phe Gly Ala Ala  
195 200 205

Ala Arg Arg Ala Val Glu Ile Ser Gly Phe Asp Ala Val Glu Ile His  
210 215 220

Gly Ala His Gly Tyr Leu Ile Asn Glu Phe Tyr Ser Pro Ile Ser Asn  
225 230 235 240

Lys Arg Thr Asp Glu Tyr Gly Gly Ser Phe Glu Asn Arg Thr Arg Phe  
245 250 255

Leu Lys Glu Val Ile Asp Ser Val Lys Ser Ser Ile Pro Asn Asp Val  
260 265 270

P03371US0 Sequence listing).txt

Pro Val Phe Leu Arg Ile Ser Ala Ala Glu Asn Ser Pro Asp Pro Glu  
275 280 285

Ala Trp Thr Ile Glu Asp Ser Lys Lys Leu Ala Asp Ile Leu Val Glu  
290 295 300

Lys Gly Ile Ala Leu Val Asp Val Ser Ser Gly Gly Asn Asp Tyr Arg  
305 310 315 320

Gln Pro Pro Arg Ser Gly Ile Ser Lys Glu Leu Arg Glu Pro Ile His  
325 330 335

Val Pro Leu Ser Arg Ala Ile Lys Gln His Val Gly Asp Lys Leu Leu  
340 345 350

Val Ser Cys Val Gly Gly Leu Glu Lys Asp Pro Glu Leu Leu Asn Lys  
355 360 365

Tyr Leu Glu Glu Gly Thr Phe Asp Leu Ala Leu Ile Gly Arg Gly Phe  
370 375 380

Leu Arg Asn Pro Gly Leu Val Trp Glu Phe Ala Asp Lys Leu Gly Val  
385 390 395 400

Arg Leu His Gln Ala Leu Gln Leu Gly Trp Gly Phe Trp Pro Asn Lys  
405 410 415

Gln Gln Ile Val Asp Leu Ile Glu Arg Thr Ser Lys Leu Glu Val Asn  
420 425 430

<210> 13  
<211> 1110  
<212> DNA  
<213> Candida albicans

<400> 13  
atggaaaaca acaatactat accggcatta tttcaaccga taaagatcag tgactcgatc 60  
acattaccta atagaattgg tgtttcacca atgtgcatgt attcatcgtc accaactgac 120  
aatcaagcca ctctgtttca tttgtttcat tatggatcat ttgctgtacg tggaccagca 180  
ttaatcattt tagagagtat ctttgtgtcc gaaaattccg gattatccat tcatgattta 240  
ggctctttgga atgatgatca agctcacagt ttacggaaaa ttgttgattt tattcatgat 300  
caagacggaa tttgctgtat acaattgaat cacgctgggc gaaagattgt tgaaggggta 360  
ccattccaac aaatacaaca tggttggcaa gaacattgtg tggggccatc tactgagcca 420  
tttagtgatt cacacaatac accacgagaa ttgactgtta atgaaataaa ttcaattgtg 480

P03371US0 Sequence listing).txt

```

gaagactttg ccaatgcagc ttggcgggct gtggaaatct caaaattcga tgccattgaa 540
atacattgtg ctaatggatg ttttaatacac caatttttaa gttaaattgac aaacaagaga 600
gctgaccaat acggggggctc atttgaaaac agagtttagat ttctttttaca aataattgag 660
aatataaaac gaaagataga aacaccgatt ttcttaaagt ttccaatgtc agataattgt 720
agtgatccgg aagcgtggtc tacggaagat gcattgaagt tggccgatct tgttattgat 780
ttaggagtaa aggtgatcga cgttacatca ggtggaaatg ttgcgcatg caaatctaga 840
tatctattaa atgacgacaa acaactacct tctcaagtgc ccttggtctg taaattgaaa 900
agccacatta gaaaccgatg tttgatcgca tgcagtggag gattagatcg agacatattt 960
aaactcgatg agttttattgc taatggtgac tttgatatag cattgatagg taaaggattt 1020
ctcaaaaaca ctggattgat cagccgtatt gctgaccaat tgcaagcaca attcagaaca 1080
gcacctcaat ataagttggc cttatcataa 1110

```

```

<210> 14
<211> 369
<212> PRT
<213> Candida albicans

```

<400> 14

```

Met Glu Asn Asn Asn Thr Ile Pro Ala Leu Phe Gln Pro Ile Lys Ile
1           5           10           15

```

```

Ser Asp Ser Ile Thr Leu Pro Asn Arg Ile Gly Val Ser Pro Met Cys
20           25           30

```

```

Met Tyr Ser Ser Ser Pro Thr Asp Asn Gln Ala Thr Leu Phe His Phe
35           40           45

```

```

Val His Tyr Gly Ser Phe Ala Val Arg Gly Pro Ala Leu Ile Ile Leu
50           55           60

```

```

Glu Ser Ile Phe Val Ser Glu Asn Ser Gly Leu Ser Ile His Asp Leu
65           70           75           80

```

```

Gly Leu Trp Asn Asp Asp Gln Ala His Ser Leu Arg Lys Ile Val Asp
85           90           95

```

```

Phe Ile His Asp Gln Asp Gly Ile Cys Cys Ile Gln Leu Asn His Ala
100          105          110

```

```

Gly Arg Lys Ile Val Glu Gly Val Pro Phe Gln Gln Ile Gln His Gly
115          120          125

```

P03371US0 Sequence listing).txt

Trp Gln Glu His Cys Val Gly Pro Ser Thr Glu Pro Phe Ser Asp Ser  
130 135 140

His Asn Thr Pro Arg Glu Leu Thr Val Asn Glu Ile Asn Ser Ile Val  
145 150 155 160

Glu Asp Phe Ala Asn Ala Ala Trp Arg Ala Val Glu Ile Ser Lys Phe  
165 170 175

Asp Ala Ile Glu Ile His Cys Ala Asn Gly Cys Leu Ile His Gln Phe  
180 185 190

Leu Ser Lys Leu Thr Asn Lys Arg Ala Asp Gln Tyr Gly Gly Ser Phe  
195 200 205

Glu Asn Arg Val Arg Phe Leu Leu Gln Ile Ile Glu Asn Ile Lys Arg  
210 215 220

Lys Ile Glu Thr Pro Ile Phe Leu Lys Phe Pro Met Ser Asp Asn Cys  
225 230 235 240

Ser Asp Pro Glu Ala Trp Ser Thr Glu Asp Ala Leu Lys Leu Ala Asp  
245 250 255

Leu Val Ile Asp Leu Gly Val Lys Val Ile Asp Val Thr Ser Gly Gly  
260 265 270

Asn Val Ala His Cys Lys Ser Arg Tyr Leu Leu Asn Asp Asp Lys Gln  
275 280 285

Leu Pro Ser Gln Val Pro Leu Ala Arg Lys Leu Lys Ser His Ile Arg  
290 295 300

Asn Arg Cys Leu Ile Ala Cys Ser Gly Gly Leu Asp Arg Asp Ile Phe  
305 310 315 320

Lys Leu Asp Glu Phe Ile Ala Asn Gly Asp Phe Asp Ile Ala Leu Ile  
325 330 335

Gly Lys Gly Phe Leu Lys Asn Thr Gly Leu Ile Ser Arg Ile Ala Asp  
340 345 350

Gln Leu Gln Ala Gln Phe Arg Thr Ala Pro Gln Tyr Lys Leu Ala Leu  
355 360 365

Ser

P03371US0 Sequence listing).txt

<210> 15  
 <211> 1305  
 <212> DNA  
 <213> Neurospora crassa

<400> 15  
 atggccgact tcacccagaa gaagacctcc tccccgcgg ccccggtgt tcccttctac 60  
 accccggccc aggtccccgc cgccggcact cccctccctt ccacccccgg cgatgtccct 120  
 actctcttca cccctctcaa gatccgtggt gttgagctcc agaaccgctt cgccgttgcg 180  
 cccatgtgca cctactctgc cgacgatggc cacatgaccg actggcacct tgtccacctg 240  
 ggctccttcg ccctccgcgg tgtccccctc accatcttcg aggccaccgg cgtcctcccc 300  
 aacggccgca tcacccccga gtgctctggt ctctggcagg actcccagat tgcgcccctc 360  
 aagcgcacg tcgactacat ccactcccag ggccagaagg ccggtatcca gcttgcccac 420  
 gccggccgca aggcctccac caaggcccc tggcactacc agcgcggcaa gagcgagctt 480  
 gccggccccg agcagggtgg ctggccccgag aacgtctggg cccccagcgc catcagctac 540  
 aacgaggaga ctttccccctt cccaaggag atgaccgtcg agcagatcca cgagctcgtc 600  
 gaggcctgga aggcgtctgc ccagcgtgcc ctcaaggccg gcttcgacct cattgagatc 660  
 cacgccgccc acggctacct catttccgag ttcttgagcc ccatctccaa ccagcgtacc 720  
 gaccagtacg gtggctcctt cgagaaccgc acccggttc tccgcgagat catctcggcc 780  
 gtccgctccg tcatccccga ggacatgccc ctcttcgtcc gtgtctccgc caccgagtgg 840  
 atggagtaca ccggccagcc ctcgtgggac ctccagcaga ccattgagct cgccaagatc 900  
 ctccccgacc tcggcgtcga cctcctcgac gtctcttccg gcggcaacaa caaggaccag 960  
 aagatcaacg tccacaccta ctaccagatc gacatggccg agcagatccg cgcggccgtg 1020  
 cacgaggccg gcaagcagct cctcgtcggg gccgtcggct tggtcacctc ggctgagatc 1080  
 gccaaggaga ccgtccagga gaaggaggat ggcagagtca ccatccagcg cgagaacggc 1140  
 gccaagactc gtgccgatat ggtccttggt gccaggcagt tcttgaagga gcccaggttc 1200  
 gtcctcactg tcgccgacga gttgggtggt gatgtcaagg cccctgttca gtacctccgt 1260  
 ggtcctctta gcagcaggcc caagaagttg accactgttc cttaa 1305

<210> 16  
 <211> 434  
 <212> PRT  
 <213> Neurospora crassa

<400> 16

Met Ala Asp Phe Thr Gln Lys Lys Thr Ser Ser Pro Ala Ala Pro Gly  
 1 5 10 15

P03371US0 Sequence listing).txt

Val Pro Phe Tyr Thr Pro Ala Gln Val Pro Ala Ala Gly Thr Pro Leu  
20 25 30

Pro Ser Thr Pro Gly Asp Val Pro Thr Leu Phe Thr Pro Leu Lys Ile  
35 40 45

Arg Gly Val Glu Leu Gln Asn Arg Phe Ala Val Ala Pro Met Cys Thr  
50 55 60

Tyr Ser Ala Asp Asp Gly His Met Thr Asp Trp His Leu Val His Leu  
65 70 75 80

Gly Ser Phe Ala Leu Arg Gly Val Pro Leu Thr Ile Phe Glu Ala Thr  
85 90 95

Gly Val Leu Pro Asn Gly Arg Ile Thr Pro Glu Cys Ser Gly Leu Trp  
100 105 110

Gln Asp Ser Gln Ile Ala Pro Leu Lys Arg Ile Val Asp Tyr Ile His  
115 120 125

Ser Gln Gly Gln Lys Ala Gly Ile Gln Leu Ala His Ala Gly Arg Lys  
130 135 140

Ala Ser Thr Lys Ala Pro Trp His Tyr Gln Arg Gly Lys Ser Glu Leu  
145 150 155 160

Ala Gly Pro Glu Gln Gly Gly Trp Pro Glu Asn Val Trp Ala Pro Ser  
165 170 175

Ala Ile Ser Tyr Asn Glu Glu Thr Phe Pro Phe Pro Lys Glu Met Thr  
180 185 190

Val Glu Gln Ile His Glu Leu Val Glu Ala Trp Lys Ala Ser Ala Gln  
195 200 205

Arg Ala Leu Lys Ala Gly Phe Asp Leu Ile Glu Ile His Ala Ala His  
210 215 220

Gly Tyr Leu Ile Ser Glu Phe Leu Ser Pro Ile Ser Asn Gln Arg Thr  
225 230 235 240

Asp Gln Tyr Gly Gly Ser Phe Glu Asn Arg Thr Arg Val Leu Arg Glu  
245 250 255

Ile Ile Ser Ala Val Arg Ser Val Ile Pro Glu Asp Met Pro Leu Phe  
260 265 270

P03371US0 Sequence listing).txt

Val Arg Val Ser Ala Thr Glu Trp Met Glu Tyr Thr Gly Gln Pro Ser  
275 280 285

Trp Asp Leu Gln Gln Thr Ile Glu Leu Ala Lys Ile Leu Pro Asp Leu  
290 295 300

Gly Val Asp Leu Leu Asp Val Ser Ser Gly Gly Asn Asn Lys Asp Gln  
305 310 315 320

Lys Ile Asn Val His Thr Tyr Tyr Gln Ile Asp Met Ala Glu Gln Ile  
325 330 335

Arg Ala Ala Val His Glu Ala Gly Lys Gln Leu Leu Val Gly Ala Val  
340 345 350

Gly Leu Val Thr Ser Ala Glu Ile Ala Lys Glu Thr Val Gln Glu Lys  
355 360 365

Glu Asp Gly Arg Val Thr Ile Gln Arg Glu Asn Gly Ala Lys Thr Arg  
370 375 380

Ala Asp Met Val Leu Val Ala Arg Gln Phe Leu Lys Glu Pro Glu Phe  
385 390 395 400

Val Leu Thr Val Ala Asp Glu Leu Gly Val Asp Val Lys Ala Pro Val  
405 410 415

Gln Tyr Leu Arg Gly Pro Leu Ser Ser Arg Pro Lys Lys Leu Thr Thr  
420 425 430

Val Pro

<210> 17

<211> 1476

<212> DNA

<213> Neurospora crassa

<400> 17

atggctactt ccactacctc cgacctcaaa ctctcccaac ccctcaccct cccaatggc	60
cttacccctcc ccaaccgcct cgtcaaagcc gccatggccg aacaaatggg cttcggcaac	120
cacctgcca accccgaact cgccgccgtc tacgccacct gggcccgcgg cgactggggc	180
ctgattctca ccggcaacgt ccaagtcgac cacgcgcaca agggcgacgc ccacgacatc	240
agccccaacc accccggcac cacgcccag cagaccgtca cggccttcaa ggcctggggc	300
gacgccgcgc gcctgaatgg ccagtccaaa acgcctgtgg tcgtgcagat caaccaccct	360

P03371US0 Sequence listing).txt

ggtcgccaga gtccgatggg cgcggggcacg cggggactgt gggagaaggc ggtggcgccc	420
tcgccggtgc cgttggtggt gggagaggcg tttgtgcctc gcttggtgtc gaaagtgtt	480
ttcggcacgc cgcgggagct gacggttgcg gagatcaagg atatcgtgca aaagtttgcg	540
gtgacggcga ggatcacggc cgaggccggg ttcaatggcg tggagatcca tgcggcgcat	600
ggatacctgt tggcgagtt cttgagcaag aagacaaaca ggcgcgggga tgagtatggc	660
gggtcggctg agaacagggc gaggattgtt ggggagatta ttaaggagtg caggaggcag	720
gtgactgagg cggtgggtga agaggaggcg aagaagtttg tggtggaat caagctgaac	780
agtgcggatt ggcaggcggg acgcgatgga aaggaggagg aggagacgga tacggcggag	840
gaggtgttga agcagattga gctttttgag cagtggggga tcgactttgt cgaggttagc	900
ggtggcagtt atgaggatcc tcaggtaagt tttggtgttg tttgagggat ggggcaagg	960
gttgctgtc gtgaacaaca aaaggggcac ggaacaaatg ctaacgccat acagatggcc	1020
aacggtccca agcccgaata gtccgaacgc accatggccc gcgaggcctt cttcctcgag	1080
ttcgccaaga tcatccgcac caagttcccc aagcttcctc tcatggtcac cggcggcttc	1140
cgcactcgtc agggcatgga ggccgctttg gaatccgatg attgcgacat gatcggtatc	1200
ggacgcccgg ccatcatcaa cccttcgctt cccgccaact tgatcctcaa cccggagggtg	1260
ccggatgcgg atgcccgtt gttcgacaag aagagggtg agccgcactg gatcgttgag	1320
aagttgggca tgaagtccat tgttggtgct ggtgttgagg tggtagctca cgttccaacc	1380
ccatttgctt cattgtgttt ccgagtatgt catgctgact tggttctttt ctagacgtgg	1440
tatgtgagcg agctcaagaa gctggccaag ttttag	1476

<210> 18  
 <211> 1314  
 <212> DNA  
 <213> *Neurospora crassa*

<400> 18	
atggctactt ccactacctc cgacctcaaa ctctcccaac ccctcacct cccaatggc	60
cttacacctcc ccaaccgcct cgtcaaagcc gccatggccg aacaaatggg cttcggcaac	120
cacctgccca accccgaact cgcgcgcgtc tacgccacct gggcccgcgg cgactggggc	180
ctgattctca ccggcaacgt ccaagtcgac cacgcgcaca agggcgacgc ccacgacatc	240
agccccaacc accccggcac cacgcccag cagaccgtca cggccttcaa ggcctgggcg	300
gacgccgcgc gcctgaatgg ccagtccaaa acgcctgtgg tcgtgcagat caaccacct	360
ggtcgccaga gtccgatggg cgcggggcacg cggggactgt gggagaaggc ggtggcgccc	420
tcgccggtgc cgttggtggt gggagaggcg tttgtgcctc gcttggtgtc gaaagtgtt	480
ttcggcacgc cgcgggagct gacggttgcg gagatcaagg atatcgtgca aaagtttgcg	540

P03371US0 Sequence listing).txt

gtgacggcga ggatcacggc cgaggccggg ttcaatggcg tggagatcca tgcggcgcac	600
ggatacctgt tggcgcagtt cttgagcaag aagacaaaca ggcgcgggga tgagtatggc	660
gggtcggctg agaacagggc gaggattgtt ggggagatta ttaaggagtg caggaggcag	720
gtgactgagg cgggtgggtga agaggaggcg aagaagtttg tgggtgggaat caagctgaac	780
agtgcggatt ggcaggcggg acgcgatgga aaggaggagg aggagacgga tacggcggag	840
gaggtgttga agcagattga gctttttgag cagtggggga tcgactttgt cgaggttagc	900
ggtggcagtt atgaggatcc tcagatggcc aacggtccca agcccgaaaa gtccgaacgc	960
accatggccc gcgaggcctt cttcctcgag ttcgccaaga tcatccgcac caagttcccc	1020
aagcttcctc tcatggtcac cggcggcttc cgcactcgtc agggcatgga ggccgctttg	1080
gaatccgatg attgcgacat gatcggatc ggacgcccgg ccatcatcaa cccttcgctt	1140
cccgccaact tgatcctcaa cccggagggtg ccggatgcgg atgcccgctt gttcgacaag	1200
aagagggctg agccgcactg gatcgttgag aagttgggca tgaagtccat tgttggtgct	1260
ggtgttgagg tgacgtggta tgtgagcgag ctcaagaagc tggccaagtt ttag	1314

<210> 19  
 <211> 437  
 <212> PRT  
 <213> Neurospora crassa

<400> 19

Met	Ala	Thr	Ser	Thr	Thr	Ser	Asp	Leu	Lys	Leu	Ser	Gln	Pro	Leu	Thr
1				5					10					15	

Leu	Pro	Asn	Gly	Leu	Thr	Leu	Pro	Asn	Arg	Leu	Val	Lys	Ala	Ala	Met
			20					25					30		

Ala	Glu	Gln	Met	Gly	Phe	Gly	Asn	His	Leu	Pro	Asn	Pro	Glu	Leu	Ala
		35					40					45			

Ala	Val	Tyr	Ala	Thr	Trp	Ala	Arg	Gly	Asp	Trp	Gly	Leu	Ile	Leu	Thr
	50					55					60				

Gly	Asn	Val	Gln	Val	Asp	His	Ala	His	Lys	Gly	Asp	Ala	His	Asp	Ile
65					70					75					80

Ser	Pro	Asn	His	Pro	Gly	Thr	Thr	Pro	Glu	Gln	Thr	Val	Thr	Ala	Phe
				85					90					95	

Lys	Ala	Trp	Ala	Asp	Ala	Ala	Arg	Leu	Asn	Gly	Gln	Ser	Lys	Thr	Pro
			100					105					110		

Val	Val	Val	Gln	Ile	Asn	His	Pro	Gly	Arg	Gln	Ser	Pro	Met	Gly	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

P03371US0 Sequence listing).txt

115

120

125

Gly Thr Arg Gly Leu Trp Glu Lys Ala Val Ala Pro Ser Pro Val Pro  
130 135 140

Leu Val Leu Gly Glu Ala Phe Val Pro Arg Leu Leu Ser Lys Val Leu  
145 150 155 160

Phe Gly Thr Pro Arg Glu Leu Thr Val Ala Glu Ile Lys Asp Ile Val  
165 170 175

Gln Lys Phe Ala Val Thr Ala Arg Ile Thr Ala Glu Ala Gly Phe Asn  
180 185 190

Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ala Gln Phe Leu  
195 200 205

Ser Lys Lys Thr Asn Arg Arg Gly Asp Glu Tyr Gly Gly Ser Ala Glu  
210 215 220

Asn Arg Ala Arg Ile Val Gly Glu Ile Ile Lys Glu Cys Arg Arg Gln  
225 230 235 240

Val Thr Glu Ala Val Gly Glu Glu Glu Ala Lys Lys Phe Val Val Gly  
245 250 255

Ile Lys Leu Asn Ser Ala Asp Trp Gln Ala Gly Arg Asp Gly Lys Glu  
260 265 270

Glu Glu Glu Thr Asp Thr Ala Glu Glu Val Leu Lys Gln Ile Glu Leu  
275 280 285

Phe Glu Gln Trp Gly Ile Asp Phe Val Glu Val Ser Gly Gly Ser Tyr  
290 295 300

Glu Asp Pro Gln Met Ala Asn Gly Pro Lys Pro Glu Lys Ser Glu Arg  
305 310 315 320

Thr Met Ala Arg Glu Ala Phe Phe Leu Glu Phe Ala Lys Ile Ile Arg  
325 330 335

Thr Lys Phe Pro Lys Leu Pro Leu Met Val Thr Gly Gly Phe Arg Thr  
340 345 350

Arg Gln Gly Met Glu Ala Ala Leu Glu Ser Asp Asp Cys Asp Met Ile  
355 360 365

P03371US0 Sequence listing).txt

Gly Ile Gly Arg Pro Ala Ile Ile Asn Pro Ser Leu Pro Ala Asn Leu  
370 375 380

Ile Leu Asn Pro Glu Val Pro Asp Ala Asp Ala Arg Leu Phe Asp Lys  
385 390 395 400

Lys Arg Ala Glu Pro His Trp Ile Val Glu Lys Leu Gly Met Lys Ser  
405 410 415

Ile Val Gly Ala Gly Val Glu Val Thr Trp Tyr Val Ser Glu Leu Lys  
420 425 430

Lys Leu Ala Lys Phe  
435

<210> 20  
<211> 1412  
<212> DNA  
<213> Magnaporthe grisea

<400> 20  
atgtcggcag aaaagaagac tttagcaaaa ccggccgccg ggggtgcctta ctacacccca 60  
gcccaggagc cgccggcagg gacccttttg cagcagcagg acgccatccc aacgctgttc 120  
aagcctctga agatccgtgg cgtcagctc tccaaccgct ttggcgtctc gcccatgtgc 180  
acctactcag ccgacgatgg ccacctgacc gacttccact tgggtgcacct gggccagttc 240  
gccctgcacg gcacggccct gaccattgtc gaggccacat ccgtcacgcc caacggacgc 300  
atctcgcccg aggacagcgg cctgtggcaa gacagccaga tcgctcctct gcgccgcatc 360  
gtcgactacg tgcacagcca gggccaaaag atcgccatcc aactgggtca tgccggccgc 420  
aaggccagca caaaggcccc ctggcacgac tccttcaccc ccagcggcga gtataagccg 480  
agagagggct tacaggctgt cggacccgag tatggcggct ggcctgatga cgtctgggcc 540  
ccgagcgcca tcccgttctc ggaggacttt ccgaacccca aggagatgac cgttgaggag 600  
attgagggac tcgtcaccag ctttgtggac gctgccaagc gtgccatcga ggccggcgtc 660  
gacattattg agattcacgg cgctcacggt tacctgatca ccgagttcct ttcgccgcta 720  
tcaaacgtaa gtggagatac tttgtgtggg gctgtgcgca tactccctcg ggtgtgactt 780  
ctattaacat tttatttcct ggcacgcaga aacggacaga caagtacggc ggcagctttg 840  
agaaccgcac ccgggtcctg atcgatatta tcaaggccgt ccgggcagtg attcccgagg 900  
agatgccact cttcgtccga atctccgcga ccgaatggat ggagtacgcc ggcgagccta 960  
gctgggacct cgagcagagc acacagcttg ccaagctcct cccggacctg ggtgtcgacc 1020  
tgctcgacgt cagctcgggc ggaaactcgg tggcccaaaa gatcgagctc acgccgtact 1080  
accagatcga cctggcagcc aagatccgcg aggccgtcgg cgatagggtg ctcataggcg 1140

P03371US0 Sequence listing).txt

cggtcggcaa catcaacacg gctgacattg cgcgcgatgt cgtggatgag cagggcgccg	1200
agaaggtggc cgaggccaag cagacgcatg acaccatcga ggtcgtgagc gaatcacatg	1260
gcggaagac caaggcggat ctggtcctca ttgctcgcca gttcctgcgc gagcctgagt	1320
ttgtgctgag gacggcgcat aaccttgggg tcaatgtgca gtggcctcac caataccaca	1380
gagcagtgtg gcgcaagggg gcaaggattt ga	1412

<210> 21  
 <211> 1329  
 <212> DNA  
 <213> Magnaporthe grisea

<400> 21	
atgtcggcag aaaagaagac tttgagcaaa ccggccgccc ggggtgcctta ctacacccca	60
gcccaggagc cgccggcagg gaccctttg cagcagcagg acgcatccc aacgctgttc	120
aagcctctga agatccgtgg cgtcgagctc tccaaccgct ttggcgcttc gcccatgtgc	180
acctactcag ccgacgatgg ccacctgacc gacttccact tgggtgcacct gggccagttc	240
gccctgcacg gcacggccct gaccattgtc gaggccacat ccgtcacgcc caacggacgc	300
atctcgcccg aggacagcgg cctgtggcaa gacagccaga tcgctcctct gcgccgcac	360
gtcgactacg tgcacagcca gggccaaaag atcgccatcc aactggctca tgccggccgc	420
aaggccagca caaaggcccc ctggcacgac tccttcaccc ccagcggcga gtataagccg	480
agagaggggt tacaggtcgt cggacccgag tatggcgggt ggcctgatga cgtctgggcc	540
ccgagcgcca tcccgttctc ggaggacttt ccgaacccca aggagatgac cgttgaggag	600
attgagggac tcgtcaccag ctttgtggac gctgccaagc gtgccatcga ggccggcgctc	660
gacattattg agattcacgg cgctcacggt tacctgatca ccgagttcct ttcgccgcta	720
tcaaacaaac ggacagacaa gtacggcggc agctttgaga accgcacccg ggtcctgac	780
gatattatca aggccgtccg ggcagtgatt cccgaggaga tgccactctt cgtccgaatc	840
tccgcgaccg aatggatgga gtacgccggc gacgctagct gggacctcga gcagagcaca	900
cagcttgcca agctcctccc ggacctgggt gtcgacctgc tcgacgtcag ctcgggcgga	960
aactcggtgg cccaaaagat cgagctcacg ccgtactacc agatcgacct ggcagccaag	1020
atccgcgagg ccgtcggcga taggttgctc ataggcgcgg tcggcaacat caacacggct	1080
gacattgctc gcgatgtcgt ggatgagcag ggcgccgaga aggtggccga ggccaagcag	1140
acgcatgaca ccatcgagggt cgtgagcgaa tcacatggcg gcaagaccaa ggcggatctg	1200
gtcctcattg ctcgccagtt cctgcgcgag cctgagtttg tgctgaggac ggcgcataac	1260
cttgggggtca atgtgcagtg gcctcaccaa taccacagag cagtgtggcg caagggtgca	1320
aggatttga	1329

P03371US0 Sequence listing).txt

<210> 22  
 <211> 442  
 <212> PRT  
 <213> Magnaporthe grisea

<400> 22

Met Ser Ala Glu Lys Lys Thr Leu Ser Lys Pro Ala Ala Gly Val Pro  
 1 5 10 15

Tyr Tyr Thr Pro Ala Gln Glu Pro Pro Ala Gly Thr Pro Leu Gln Gln  
 20 25 30

Gln Asp Ala Ile Pro Thr Leu Phe Lys Pro Leu Lys Ile Arg Gly Val  
 35 40 45

Glu Leu Ser Asn Arg Phe Gly Val Ser Pro Met Cys Thr Tyr Ser Ala  
 50 55 60

Asp Asp Gly His Leu Thr Asp Phe His Leu Val His Leu Gly Gln Phe  
 65 70 75 80

Ala Leu His Gly Thr Ala Leu Thr Ile Val Glu Ala Thr Ser Val Thr  
 85 90 95

Pro Asn Gly Arg Ile Ser Pro Glu Asp Ser Gly Leu Trp Gln Asp Ser  
 100 105 110

Gln Ile Ala Pro Leu Arg Arg Ile Val Asp Tyr Val His Ser Gln Gly  
 115 120 125

Gln Lys Ile Ala Ile Gln Leu Ala His Ala Gly Arg Lys Ala Ser Thr  
 130 135 140

Lys Ala Pro Trp His Asp Ser Phe Thr Pro Ser Gly Glu Tyr Lys Pro  
 145 150 155 160

Arg Glu Gly Leu Gln Val Val Gly Pro Glu Tyr Gly Gly Trp Pro Asp  
 165 170 175

Asp Val Trp Ala Pro Ser Ala Ile Pro Phe Ser Glu Asp Phe Pro Asn  
 180 185 190

Pro Lys Glu Met Thr Val Glu Glu Ile Glu Gly Leu Val Thr Ser Phe  
 195 200 205

Val Asp Ala Ala Lys Arg Ala Ile Glu Ala Gly Val Asp Ile Ile Glu  
 210 215 220

P03371US0 Sequence listing).txt

Ile His Gly Ala His Gly Tyr Leu Ile Thr Glu Phe Leu Ser Pro Leu  
225 230 235 240

Ser Asn Lys Arg Thr Asp Lys Tyr Gly Gly Ser Phe Glu Asn Arg Thr  
245 250 255

Arg Val Leu Ile Asp Ile Ile Lys Ala Val Arg Ala Val Ile Pro Glu  
260 265 270

Glu Met Pro Leu Phe Val Arg Ile Ser Ala Thr Glu Trp Met Glu Tyr  
275 280 285

Ala Gly Glu Pro Ser Trp Asp Leu Glu Gln Ser Thr Gln Leu Ala Lys  
290 295 300

Leu Leu Pro Asp Leu Gly Val Asp Leu Leu Asp Val Ser Ser Gly Gly  
305 310 315 320

Asn Ser Val Ala Gln Lys Ile Glu Leu Thr Pro Tyr Tyr Gln Ile Asp  
325 330 335

Leu Ala Ala Lys Ile Arg Glu Ala Val Gly Asp Arg Leu Leu Ile Gly  
340 345 350

Ala Val Gly Asn Ile Asn Thr Ala Asp Ile Ala Arg Asp Val Val Asp  
355 360 365

Glu Gln Gly Ala Glu Lys Val Ala Glu Ala Lys Gln Thr His Asp Thr  
370 375 380

Ile Glu Val Val Ser Glu Ser His Gly Gly Lys Thr Lys Ala Asp Leu  
385 390 395 400

Val Leu Ile Ala Arg Gln Phe Leu Arg Glu Pro Glu Phe Val Leu Arg  
405 410 415

Thr Ala His Asn Leu Gly Val Asn Val Gln Trp Pro His Gln Tyr His  
420 425 430

Arg Ala Val Trp Arg Lys Gly Ala Arg Ile  
435 440

<210> 23  
<211> 1188  
<212> DNA  
<213> Schizosaccharomyces pombe

P03371US0 Sequence listing).txt

```

<400> 23
atgactattg ttaatgaagg agccgaaaat gttggttatt ttacacctgc gcaaaaaata    60
ccagctggag cggcgatagg tgtaccgcaa acaaaattat ttactcctct taaaattaga    120
ggagtggagt tccataacag aatgtttgtt tcgccgatgt gcacttattc cgctgaccaa    180
gaagggcatt tgacagattt tcacctagta catcttggag cgatgggaat gcgtgggcct    240
ggccttgtaa tggtagaagc gacagcgggt tccccagagg gacgaatttc acctaattgat    300
tcaggattat ggatggagtc gcaaatgaag ccgttacgaa gaattgttga atttgctcat    360
tcgcaaaatc aaaaaattgg gattcaattg gcgcatgctg gtagaaaggc tagcaccact    420
gctccttattc gaggatacac agttgcgact gaagctcaag gtgggtggga gaatgatgtt    480
tatggaccaa atgaagacag gtgggacgaa aaccacgctc aacctcataa gttaactgaa    540
aagcaatatg atgaattagt ggataagttt gttgttgctg cgaagcgtgc agttgaaata    600
ggttttgatg taattgaaat tcatggcgct catgggttatc ttatatcgtc aacagttagt    660
cctgccacta atgaccgcaa tgacaagtat ggtgggacat ttgagaaacg tattttgttt    720
cctatggaag ttgtccattc tgttcgtaaa gcaattccag atagtatgcc cttgttttat    780
agagtaacgg ctacagattg gttgcccaa ggacaaggat gggagataga agatacagtt    840
gcattagcag cgaggcttcg cgatgggtgg gttgacttga tagatgttag ctctgggtgg    900
aatcacaagg atcaaagaat tgaggtgaag gattgctatc aagttccttt tgcggaaaag    960
attaaggatc aagtgaatgg aatactactt ggcgctgtcg gaatgatcag ggatgggtctt   1020
acggcgaaatg aaatcctaga aagtggaaaa gctgatgtta cttttgtcgc aagggagttc   1080
ttaaggaacc cgtcgttggg gctagacagc gcgaaccagt tgggtgaaaa tgttgcatgg   1140
ccagttcagt atgactatgc agttaaggga cacagaaagt tacgttga                   1188

```

```

<210> 24
<211> 407
<212> PRT
<213> Schizosaccharomyces pombe

```

<400> 24

```

Met Thr Ile Val Asn Glu Gly Ala Glu Asn Val Gly Tyr Phe Thr Pro
1           5           10          15

```

```

Ala Gln Lys Ile Pro Ala Gly Ala Ala Ile Gly Val Pro Gln Thr Lys
          20          25          30

```

```

Leu Phe Thr Pro Leu Lys Ile Arg Gly Val Glu Phe His Phe Thr Asn
          35          40          45

```

```

Arg Met Phe Val Ser Pro Met Cys Thr Tyr Ser Ala Asp Gln Glu Gly
          50          55          60

```

P03371US0 Sequence listing).txt

His Leu Thr Asp Phe His Leu Val His Leu Gly Ala Met Gly Met Arg  
65 70 75 80

Gly Pro Gly Leu Val Met Val Glu Ala Thr Ala Val Ser Pro Glu Gly  
85 90 95

Arg Ile Ser Pro Asn Asp Ser Gly Leu Trp Phe Thr Met Glu Ser Gln  
100 105 110

Met Lys Pro Leu Arg Arg Ile Val Glu Phe Ala His Ser Gln Asn Gln  
115 120 125

Lys Ile Gly Ile Gln Leu Ala His Ala Gly Arg Lys Ala Ser Thr Thr  
130 135 140

Ala Pro Tyr Arg Gly Tyr Thr Val Ala Thr Glu Ala Gln Gly Gly Trp  
145 150 155 160

Glu Asn Asp Val Tyr Gly Pro Phe Thr Asn Glu Asp Arg Trp Asp Glu  
165 170 175

Asn His Ala Gln Pro His Lys Leu Thr Glu Lys Gln Tyr Asp Glu Leu  
180 185 190

Val Asp Lys Phe Val Val Ala Ala Lys Arg Ala Val Glu Ile Gly Phe  
195 200 205

Asp Val Ile Glu Ile His Gly Ala His Gly Tyr Leu Ile Ser Ser Thr  
210 215 220

Val Ser Pro Ala Phe Thr Thr Asn Asp Arg Asn Asp Lys Tyr Gly Gly  
225 230 235 240

Thr Phe Glu Lys Arg Ile Leu Phe Pro Met Glu Val Val His Ser Val  
245 250 255

Arg Lys Ala Ile Pro Asp Ser Met Pro Leu Phe Tyr Arg Val Thr Ala  
260 265 270

Thr Asp Trp Leu Pro Lys Gly Gln Gly Trp Glu Ile Glu Asp Thr Val  
275 280 285

Ala Phe Thr Leu Ala Ala Arg Leu Arg Asp Gly Gly Val Asp Leu Ile  
290 295 300

Asp Val Ser Ser Gly Gly Asn His Lys Asp Gln Arg Ile Glu Val Lys

P03371US0 Sequence listing).txt

305 310 315 320

Asp Cys Tyr Gln Val Pro Phe Ala Glu Lys Ile Lys Asp Gln Val Asn  
325 330 335

Gly Ile Leu Leu Gly Ala Val Gly Met Ile Arg Asp Gly Leu Phe Thr  
340 345 350

Thr Ala Asn Glu Ile Leu Glu Ser Gly Lys Ala Asp Val Thr Phe Val  
355 360 365

Ala Arg Glu Phe Leu Arg Asn Pro Ser Leu Val Leu Asp Ser Ala Asn  
370 375 380

Gln Leu Gly Glu Asn Val Ala Trp Pro Val Gln Tyr Asp Tyr Ala Val  
385 390 395 400

Lys Gly His Arg Lys Leu Arg  
405

<210> 25  
<211> 777  
<212> DNA  
<213> Colletotrichium trifolii

<400> 25  
cgaaacctcg acccaaacaa acagctgacc ctctccttga caacaaagcc ggccatcctc 60  
gccgacgatt gcctctaccc ccgcatagtc aactcgcac gtccgttctc ccaccgtcaa 120  
acagacagca tgacgggcac cgcgaacaag gccgcccccg gtgtgccgtt ttacaccccg 180  
gcccaggagc ctcccgcggg aacgccagtc gacgccagca cggctccgac gctcttcaag 240  
cccctccgca tccgcgacct caccatcaac aaccgcatct gggtcagccc catgtgccag 300  
tactccgccg acaatggcca cgcgaccgac taccacctcg tccacctggg ccagttcgcc 360  
ctgcacggcg ccgccctgtc catggctgag gccaccgccg tcgaggctcg tggccgcatc 420  
tccccgagg atgtcggttt gtggcaggac tcgcagattg cgccgctgaa gcgcatcgtc 480  
gactttatcc actcgcagaa ccaggtcgcg gccatccagc tcgcccacgc cggtcgcaag 540  
gctagcacc tgccaccgtg gatcaccgag gctcgcggca aggcgctggc tcaggagagc 600  
gagaacggct ggcccgcga cgttggtggc cccagcgcga ttccttacac caaggactgg 660  
gccacaccgc gtgagttgac taccgaggrr gtcgagggc tgggtgaaga agttcgccga 720  
gtcggccaag aggtcaaac gagctggttt tgacgtcatt gagatccacg ccgctca 777

<210> 26  
<211> 645  
<212> DNA

<213> Colletotrichium trifolii

<400> 26  
atgacgggca ccgcaacaa ggccgcccc ggtgtgccgt ttacacccc ggcccaggag 60  
cctcccgcgg gaacgccagt cgacgccagc acggctccga cgctcttcaa gcccctccgc 120  
atccgcgacc tcaccatcaa caaccgcata tgggtcagcc ccatgtgcca gtactccgcc 180  
gacaatggcc acgcgaccga ctaccacctc gtccacctgg gccagttcgc cctgcacggc 240  
gccgccctgt ccatggtcga ggccaccgcc gtcgaggctc gtggccgcat ctcccccgag 300  
gatgtcggtt tgtggcagga ctgcgagatt gcgccgctga agcgcatcgt cgactttatc 360  
cactcgaga accaggtcgc ggccatccag ctgcccacg ccggtcgcaa ggctagcacc 420  
ctggcaccgt ggatcaccga ggctcgcggc aaggcgctgg ctcaggagag cgagaacggc 480  
tggcccgcgc acgttgtggc tcccagcgcg attccttaca ccaaggactg ggccacaccg 540  
cgtgagttga ctaccaggr gtcgagggtc tgggtgaaga agttcgccga gtcggccaag 600  
aggtcaaata gagctggttt tgacgtcatt gagatccacg ccgct 645

<210> 27

<211> 215

<212> PRT

<213> Colletotrichium trifolii

<220>

<221> misc\_feature

<222> (187)..(187)

<223> Xaa can be any naturally occurring amino acid

<400> 27

Met Thr Gly Thr Ala Asn Lys Ala Ala Pro Gly Val Pro Phe Tyr Thr  
1 5 10 15

Pro Ala Gln Glu Pro Pro Ala Gly Thr Pro Val Asp Ala Ser Thr Ala  
20 25 30

Pro Thr Leu Phe Lys Pro Leu Arg Ile Arg Asp Leu Thr Ile Asn Asn  
35 40 45

Arg Ile Trp Val Ser Pro Met Cys Gln Tyr Ser Ala Asp Asn Gly His  
50 55 60

Ala Thr Asp Tyr His Leu Val His Leu Gly Gln Phe Ala Leu His Gly  
65 70 75 80

Ala Ala Leu Ser Met Val Glu Ala Thr Ala Val Glu Ala Arg Gly Arg  
85 90 95

P03371US0 Sequence listing).txt

Ile Ser Pro Glu Asp Val Gly Leu Trp Gln Asp Ser Gln Ile Ala Pro  
100 105 110

Leu Lys Arg Ile Val Asp Phe Ile His Ser Gln Asn Gln Val Ala Ala  
115 120 125

Ile Gln Leu Ala His Ala Gly Arg Lys Ala Ser Thr Leu Ala Pro Trp  
130 135 140

Ile Thr Glu Ala Arg Gly Lys Ala Leu Ala Gln Glu Ser Glu Asn Gly  
145 150 155 160

Trp Pro Asp Asp Val Val Ala Pro Ser Ala Ile Pro Tyr Thr Lys Asp  
165 170 175

Trp Ala Thr Pro Arg Glu Leu Thr Thr Glu Xaa Ser Arg Val Trp Val  
180 185 190

Lys Lys Phe Ala Glu Ser Ala Lys Arg Ser Asn Arg Ala Gly Phe Asp  
195 200 205

Val Ile Glu Ile His Ala Ala  
210 215

<210> 28  
<211> 803  
<212> DNA  
<213> Fusarium sporotrichioides

<400> 28  
gaactgctgt agatgtggtt gaattggtat attagaccgg agtactctat atgcgagaga 60  
ctatacattg aagttgccaa cgttcttcca gattgattaa tcatggctta cgagataatc 120  
gacaacgttg cggctgaagg ggttccatat tacacaccgg ctcaagacc gccagctggt 180  
acgcagacaa gcggctcaac gaagctattc acacccatca ccatccgcgg cgtcacattc 240  
ccaaaccgcc tcttccttgc cctctcttgc caatactccg ccaaagatgg ttatgccact 300  
gattggcact tgactcacct cgggggaata atccaaagag gccccggatt gtccatggtg 360  
gaggctaccg ctgtacaaaa ccacggtcgc atcacacctc aggatgttgg tctgtgggaa 420  
gacggccaga tcgagcctct gaagcgcata accactttcg cgcacagtca gagccagaaa 480  
attggtatcc agctgtcgca tgcgggtcgc aaggccagtt gcgtatctcc ctggctaagc 540  
gtaaatgctg tcgcggcgga agaagtgggt ggctggccag acaatatcgt tgctccctcg 600  
gccatcgcac aagaaaatgg tgtgaacca gttcccaagg ctttcacgaa ggaggatata 660  
gagcaactca agagcgacta cgtggaagcg gcaaaacgag ccatccatgc tggtttcgat 720  
gttatcga aa ttcatgcagc tcatggatat ctactgcata aattcttgag tccggtaagc 780

P03371US0 Sequence listing).txt

aatcaaagaa ccgacgagta tgg 803

<210> 29  
<211> 701  
<212> DNA  
<213> Fusarium sporotrichioides

<400> 29  
atggcttacg agataatcga caacgttgcg gctgaagggg ttccatatta cacaccggct 60  
caagacccgc cagctggtac gcagacaagc ggctcaacga agctattcac acccatcacc 120  
atccgcggcg tcacattccc aaaccgcctc ttcttgccc ctctctgcca atactccgcc 180  
aaagatggtt atgccactga ttggcacttg actcacctcg ggggaataat ccaaagaggc 240  
cccgattgt ccatggtgga ggctaccgct gtacaaaacc acggtcgcac cacacctcag 300  
gatgttggtc tgtgggaaga cggccagatc gagcctctga agcgcacac cactttcgcg 360  
cacagtcaga gccagaaaat tggatccag ctgtcgcacg cgggtcgcaa ggccagttgc 420  
gtatctccct ggctaagcgt aaatgctgtc gcggcggaag aagtgggtgg ctggccagac 480  
aatatcggtt ctccctcggc catcgacaaa gaaaatggtg tgaaccagc tccaaggct 540  
ttcacgaagg aggatataga gcaactcaag agcgactacg tggaagcggc aaaacgagcc 600  
atccatgctg gtttcgatgt tatcgaaatt catgcagctc atggatatct actgcatcaa 660  
ttcttgagtc cggtagcaa tcaaagaacc gacgagtatg g 701

<210> 30  
<211> 233  
<212> PRT  
<213> Fusarium sporotrichioides

<400> 30

Met Ala Tyr Glu Ile Ile Asp Asn Val Ala Ala Glu Gly Val Pro Tyr  
1 5 10 15

Tyr Thr Pro Ala Gln Asp Pro Pro Ala Gly Thr Gln Thr Ser Gly Ser  
20 25 30

Thr Lys Leu Phe Thr Pro Ile Thr Ile Arg Gly Val Thr Phe Pro Asn  
35 40 45

Arg Leu Phe Leu Ala Pro Leu Cys Gln Tyr Ser Ala Lys Asp Gly Tyr  
50 55 60

Ala Thr Asp Trp His Leu Thr His Leu Gly Gly Ile Ile Gln Arg Gly  
65 70 75 80

Pro Gly Leu Ser Met Val Glu Ala Thr Ala Val Gln Asn His Gly Arg  
Page 34

Ile Thr Pro Gln Asp Val Gly Leu Trp Glu Asp Gly Gln Ile Glu Pro  
 100 105 110

Leu Lys Arg Ile Thr Thr Phe Ala His Ser Gln Ser Gln Lys Ile Gly  
 115 120 125

Ile Gln Leu Ser His Ala Gly Arg Lys Ala Ser Cys Val Ser Pro Trp  
 130 135 140

Leu Ser Val Asn Ala Val Ala Ala Glu Glu Val Gly Gly Trp Pro Asp  
 145 150 155 160

Asn Ile Val Ala Pro Ser Ala Ile Ala Gln Glu Asn Gly Val Asn Pro  
 165 170 175

Val Pro Lys Ala Phe Thr Lys Glu Asp Ile Glu Gln Leu Lys Ser Asp  
 180 185 190

Tyr Val Glu Ala Ala Lys Arg Ala Ile His Ala Gly Phe Asp Val Ile  
 195 200 205

Glu Ile His Ala Ala His Gly Tyr Leu Leu His Gln Phe Leu Ser Pro  
 210 215 220

Val Ser Asn Gln Arg Thr Asp Glu Tyr  
 225 230

<210> 31  
 <211> 631  
 <212> DNA  
 <213> Fusarium sporotrichioides

<400> 31  
 tttggatggt ataataataa ttctatttgt gaaacatacg gggctggtct tgatcaagaa 60  
 cgggtccatct atggtctata aagaactctt gttcactttc tttccacgtc ctttgaagct 120  
 ccaatcaatc tggttcgcca tcttgacctc cagccaagc tcgtagcaa aagctcgaac 180  
 cagaccagga ttctgttgga accaacgtcc agccctcaca atgtcgatac cagattgcaa 240  
 aacctcttca gcaagatgtc cagtcttgat tccacctact gctgaaacaa gtacactatc 300  
 gccaacagcc ttctttacct gtttggcgag gtctacctgg taagcaggac cggacttgat 360  
 ggcgatggcg gacttaggat ggataccgcc tgagctgacg tccaccaagt ctactccatg 420  
 cttgggcaag atacgcgcga gttgacaagt ctgctcgact gtccagcttt caggaaactc 480  
 gtctttgaat tgagagtcaa actcgaacca atcagttgca ctgacacgaa cgaggacagg 540

P03371US0 Sequence listing).txt

tgtagtttcg gggatggcag cgcggatgag gtcaaggatt tccaagacaa ctctgatacg 600  
gttctcgaaa ctgccaccat actcgtcggt t 631

<210> 32  
<211> 556  
<212> DNA  
<213> *Fusarium sporotrichioides*

<400> 32  
aaccgacgag tatggtggca gtttcgagaa ccgtatcaga gttgtcttgg aaatccttga 60  
cctcatccgc gctgccatcc ccgaaactac acctgtcctc gttcgtgtca gtgcaactga 120  
ttggttcgag tttgactctc aattcaaaga cgagtttcct gaaagctgga cagtcgagca 180  
gacttggtcaa ctgcgcgta tcttgcccaa gcatggagta gacttggtgg acgtcagctc 240  
aggcggatc catcctaagt ccgccatcgc catcaagtcc ggtcctgctt accaggtaga 300  
cctcgccaaa caggtaaaga aggctgttgg cgatagtgtta cttgtttcag cagtaggtgg 360  
aatcaagact ggacatcttg ctgaagaggt tttgcaatct ggtatcgaca ttgtgagggc 420  
tggacgttgg ttccaacaga atcctggtct ggttcgagct tttgctaacg agcttggcgt 480  
ggaggtcaag atggcgaacc agattgattg gagcttcaag ggacgtggaa agaaagtga 540  
caagagttct ttatag 556

<210> 33  
<211> 184  
<212> PRT  
<213> *Fusarium sporotrichioides*

<400> 33

Thr Asp Glu Tyr Gly Gly Ser Phe Glu Asn Arg Ile Arg Val Val Leu  
1 5 10 15

Glu Ile Leu Asp Leu Ile Arg Ala Ala Ile Pro Glu Thr Thr Pro Val  
20 25 30

Leu Val Arg Val Ser Ala Thr Asp Trp Phe Glu Phe Asp Ser Gln Phe  
35 40 45

Lys Asp Glu Phe Pro Glu Ser Trp Thr Val Glu Gln Thr Cys Gln Leu  
50 55 60

Ala Arg Ile Leu Pro Lys His Gly Val Asp Leu Val Asp Val Ser Ser  
65 70 75 80

Gly Gly Ile His Pro Lys Ser Ala Ile Ala Ile Lys Ser Gly Pro Ala  
85 90 95

P03371US0 Sequence listing).txt

Tyr Gln Val Asp Leu Ala Lys Gln Val Lys Lys Ala Val Gly Asp Ser  
100 105 110

Val Leu Val Ser Ala Val Gly Gly Ile Lys Thr Gly His Leu Ala Glu  
115 120 125

Glu Val Leu Gln Ser Gly Ile Asp Ile Val Arg Ala Gly Arg Trp Phe  
130 135 140

Gln Gln Asn Pro Gly Leu Val Arg Ala Phe Ala Asn Glu Leu Gly Val  
145 150 155 160

Glu Val Lys Met Ala Asn Gln Ile Asp Trp Ser Phe Lys Gly Arg Gly  
165 170 175

Lys Lys Val Asn Lys Ser Ser Leu  
180

<210> 34  
<211> 657  
<212> DNA  
<213> Fusarium sporotrichioides

<400> 34  
aggaagttgc atgtcacttg tagtgacagg gcgtcgtgta aattttataa atacctatac 60  
ttgtttgttc acttctatgc tactcatatc aatccgagaa gatcaaacag tcccctatac 120  
acacttgatca agacctatct attattttcaa aaatcagcaa tatggctgag acaatgccta 180  
agtgtgaggc aaatggccat cacaaaatca tcatcaataa ggaagctccg aatgttcctt 240  
tctatactcc agtgcaagat ccaccagcag gaacgtctta cgatgttcag cctgaaggaa 300  
gcctattctc tcttattaaa ataagaaacc tgactcttca aaaccggatt tttgtctccc 360  
caatgtgtca atattcagca aaggatggtg tcatgacccc ctggcacaaa caacacctgg 420  
gcagcttcgc agcacgaggt ccgggtctca ttgtcacaga agtcaacgca gtttcaccag 480  
agggacgaat cagtcctgag gatgcaggca tctacgatga tgggcagctt ggacctctcc 540  
gggatattgt ggactttgta cacagccagg gcgccaagat tgctattcag ataggtcatg 600  
ctgggagaaa agcgagcaca gtcgtaccgt ggctggaccg caagaacact gcttttta 657

<210> 35  
<211> 161  
<212> PRT  
<213> Fusarium sporotrichioides

<400> 35  
Met Pro Lys Cys Glu Ala Asn Gly His His Lys Ile Ile Ile Asn Lys  
1 5 10 15

P03371US0 Sequence listing).txt

Glu Ala Pro Asn Val Pro Phe Tyr Thr Pro Val Gln Asp Pro Pro Ala  
20 25 30

Gly Thr Ser Tyr Asp Val Gln Pro Glu Gly Ser Leu Phe Ser Leu Ile  
35 40 45

Lys Ile Arg Asn Leu Thr Leu Gln Asn Arg Ile Phe Val Ser Pro Met  
50 55 60

Cys Gln Tyr Ser Ala Lys Asp Gly Val Met Thr Pro Trp His Lys Gln  
65 70 75 80

His Leu Gly Ser Phe Ala Ala Arg Gly Pro Gly Leu Ile Val Thr Glu  
85 90 95

Val Asn Ala Val Ser Pro Glu Gly Arg Ile Ser Pro Glu Asp Ala Gly  
100 105 110

Ile Tyr Asp Asp Gly Gln Leu Gly Pro Leu Arg Asp Ile Val Asp Phe  
115 120 125

Val His Ser Gln Gly Ala Lys Ile Ala Ile Gln Ile Gly His Ala Gly  
130 135 140

Arg Lys Ala Ser Thr Val Val Pro Trp Leu Asp Arg Lys Asn Thr Ala  
145 150 155 160

Phe

<210> 36  
<211> 744  
<212> DNA  
<213> Fusarium graminearum

<400> 36  
gcacgagggg ttattgacaa catcgcggtc gaaggggctc cctactacac gcctgctcaa 60  
gacyctccag caggcacaca gaccagcggc tcaaccaagg ttttcacacb catcaccatc 120  
cgaggcgtca cattcccaaa ccgtctcttt cttgcccctc tctgtcaata ctccgcaaaa 180  
gatggatatg ctactgattg gcacttgact catctcggag gcattatcca acgaggcccc 240  
ggactgtcca tggtagaggc caccgctgtt caaaaccacg gtcgcatcac gcctcaggac 300  
gttggtctct gggaagatgg acaaatcgag ccctttgaag cgcatacta cttttgcccc 360  
cagccaaagc wcagaagatt ggtattcagc tctcgcacgc tggtcgtaag gctagttgtg 420  
tatctccgtg gttgagcatc aacgctgttg ccgctaagga agtcggtggc tggccagaca 480

P03371US0 Sequence listing).txt

acattgttgc tccttctgcc atcgcacaaag aagctggcgt gaaccctgtt cccaaggcct	540
tcaccaagga ggatatcgag gaactcaaga atgactttct ggctgcagcm aaacgagcca	600
wccgcgctgg ttttgatgtc atcgagatcc atgcagctca tggatacttg cttcaccagt	660
tcttgagtcc agtcagtaac caaagaaccg atgagtatgg tggcagcttc gagaaccgta	720
tcagagtcgt cttggagatc attg	744

<210> 37  
 <211> 742  
 <212> DNA  
 <213> Fusarium graminearum

<400> 37	
gcacgaggga ttattgacaa catcgcggtc gaaggggctc cctactacac gcctgctcaa	60
gacyctccag caggcacaca gaccagcggc tcaaccaagg ttttcacacb catcaccatc	120
cgaggcgtca cattcccaaa ccgtctcttt cttgcccctc tctgtcaata ctccgcaaaa	180
gatggatatg ctactgattg gcacttgact catctcggag gcattatcca acgaggcccg	240
ggactgtcca tggtagaggc caccgctgtt caaaaccacg gtcgcatcac gcctcaggac	300
gttggtctct gggaagatgg acaaatcgag cccttgaagc gcatcactac ttttgccac	360
agccaaagcc agaagattgg tattcagctc tcgcacgctg gtcgtaaggc tagttgtgta	420
tctccgtggt tgagcatcaa cgctgttgcc gctaaggaag tcggtggctg gccagacaac	480
attgttgctc cttctgccat cgcacaagaa gctggcgtga accctgttcc caaggccttc	540
accaaggagg atatcgagga actcaagaat gactttctgg ctgcagcmaa acgagccawc	600
cgcgctggtt ttgatgtcat cgagatccat gcagctcatg gatacttgct tcaccagttc	660
ttgagtccag tcagtaacca aagaaccgat gagtatggtg gcagcttcga gaaccgtatc	720
agagtcgtct tggagatcat tg	742

<210> 38  
 <211> 247  
 <212> PRT  
 <213> Fusarium graminearum

<220>  
 <221> misc\_feature  
 <222> (22)..(22)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
 <221> misc\_feature  
 <222> (37)..(37)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
 <221> misc\_feature  
 <222> (196)..(196)

P03371US0 Sequence listing).txt

<223> xaa can be any naturally occurring amino acid

<220>

<221> misc\_feature

<222> (200)..(200)

<223> xaa can be any naturally occurring amino acid

<220>

<221> misc\_feature

<222> (216)..(216)

<223> xaa can be any naturally occurring amino acid

<400> 38

Ala Arg Gly Ile Ile Asp Asn Ile Ala Ala Glu Gly Ala Pro Tyr Tyr  
1 5 10 15

Thr Pro Ala Gln Asp Xaa Pro Ala Gly Thr Gln Thr Ser Gly Ser Thr  
20 25 30

Lys Val Phe Thr Xaa Ile Thr Ile Arg Gly Val Thr Phe Pro Asn Arg  
35 40 45

Leu Phe Leu Ala Pro Leu Cys Gln Tyr Ser Ala Lys Asp Gly Tyr Ala  
50 55 60

Thr Asp Trp His Leu Thr His Leu Gly Gly Ile Ile Gln Arg Gly Pro  
65 70 75 80

Gly Leu Ser Met Val Glu Ala Thr Ala Val Gln Asn His Gly Arg Ile  
85 90 95

Thr Pro Gln Asp Val Gly Leu Trp Glu Asp Gly Gln Ile Glu Pro Leu  
100 105 110

Lys Arg Ile Thr Thr Phe Ala His Ser Gln Ser Gln Lys Ile Gly Ile  
115 120 125

Gln Leu Ser His Ala Gly Arg Lys Ala Ser Cys Val Ser Pro Trp Leu  
130 135 140

Ser Ile Asn Ala Val Ala Ala Lys Glu Val Gly Gly Trp Pro Asp Asn  
145 150 155 160

Ile Val Ala Pro Ser Ala Ile Ala Gln Glu Ala Gly Val Asn Pro Val  
165 170 175

Pro Lys Ala Phe Thr Lys Glu Asp Ile Glu Glu Leu Lys Asn Asp Phe  
180 185 190

Leu Ala Ala Xaa Lys Arg Ala Xaa Arg Ala Gly Phe Asp Val Ile Glu  
Page 40

195

Ile His Ala Ala His Gly Tyr Xaa Leu His Gln Phe Leu Ser Pro Val  
210 215 220

Ser Asn Gln Arg Thr Asp Glu Tyr Gly Gly Ser Phe Glu Asn Arg Ile  
225 230 235 240

Arg Val Val Leu Glu Ile Ile  
245

<210> 39  
<211> 647  
<212> DNA  
<213> Mycosphaerella graminicola

<400> 39  
cctcaagatc cgaggtctta ccctccagaa ccgtattatg ttgagggggc tctgccagta 60  
ctctgctccc gacggacact acacaatgtg gcatcacacc cacatgggcg gcatcatcca 120  
acgcggtccc ggactcacct gcgttgaagc cacagccgtg actcctcaag gtcgcatcac 180  
gcctgaagac gtcggtatct ggcaagattc tcagatcgag cctcttgcca aggtcgtcga 240  
gtttgcccac tcccagaacc agaagatcat gattcagttg gcgcatgcgg gccgcaaagc 300  
gagcactgtg gcaccatggt taagcggcgg cgatgttgct ggtgaggacg tcaacggatg 360  
gccacaggat gtctgggcgc ccagtgcgat tccatggaac gagaagcacg ctgtcccaaa 420  
ggagatgtcg ttggatgata tcgaggcttt caagaaggcg tttggagagg cggtaagcg 480  
ggcattgaag gctggatttg atgttattga gattcacaat gtcacggat acctcctcca 540  
cgaattcatc tgcctgagag caacaccagg accgacaagt acgggcggaa gctgggaaaa 600  
ccgcactcgt ctgacaatgg aaagtcgtcg acctgtgccg cagcatt 647

<210> 40  
<211> 215  
<212> PRT  
<213> Mycosphaerella graminicola

<400> 40

Leu Lys Ile Arg Gly Leu Thr Leu Gln Asn Arg Ile Met Leu Arg Gly  
1 5 10 15

Leu Cys Gln Tyr Ser Ala Pro Asp Gly His Tyr Thr Met Trp His His  
20 25 30

Thr His Met Gly Gly Ile Ile Gln Arg Gly Pro Gly Leu Thr Cys Val  
35 40 45

P03371US0 Sequence listing).txt

Glu Ala Thr Ala Val Thr Pro Gln Gly Arg Ile Thr Pro Glu Asp Val  
50 55 60

Gly Ile Trp Gln Asp Ser Gln Ile Glu Pro Leu Ala Lys Val Val Glu  
65 70 75 80

Phe Ala His Ser Gln Asn Gln Lys Ile Met Ile Gln Leu Ala His Ala  
85 90 95

Gly Arg Lys Ala Ser Thr Val Ala Pro Trp Leu Ser Gly Gly Asp Val  
100 105 110

Ala Gly Glu Asp Val Asn Gly Trp Pro Gln Asp Val Trp Ala Pro Ser  
115 120 125

Ala Ile Pro Trp Asn Glu Lys His Ala Val Pro Lys Glu Met Ser Leu  
130 135 140

Asp Asp Ile Glu Ala Phe Lys Lys Ala Phe Gly Glu Ala Val Lys Arg  
145 150 155 160

Ala Leu Lys Ala Gly Phe Asp Val Ile Glu Ile His Asn Ala His Gly  
165 170 175

Tyr Leu Leu His Glu Phe Ile Cys Leu Arg Ala Thr Pro Gly Pro Thr  
180 185 190

Ser Thr Gly Gly Ser Trp Glu Asn Arg Thr Arg Leu Thr Met Glu Ser  
195 200 205

Arg Arg Pro Cys Pro Gln His  
210 215

<210> 41  
<211> 560  
<212> DNA  
<213> Mycosphaerella graminicola

<400> 41  
gactgccgag taaacgcgcc ggcaaggagg cgggaggatg gccggaggat gttgtgggctc 60  
cgtcgggttg ggaggacttt acgtgggatg agaggtcctc gagcgaccct agtggaggct 120  
actatgcgcc gagagagttg tcggtcagag agatcaagga gatggtccaa gactgggcga 180  
cagcagcgaa aagggcgggtg aaagcgggcg tggatgtaat cgaaatccac ggcgcgcatg 240  
ggtacctcat ccacgaattc ctctcaccca ttaccaaccg ccggacagat tcttacggcg 300  
gttctttcga aaaccgtacc cgtctactca ttgaaatcgt aacagccgctc cgagccgcga 360  
tgccctccag catgcctctc ttctccgcc tctcctctac agaattggatg gaagataccg 420

P03371US0 Sequence listing).txt

acatcggcaa gaagttcggga agctgggatg tcgaaagcac gatcaagatc tccaaaatcc 480  
 tggccgactt gggcgttgat ctctcgacg tgtcttccgg tgggaatcat cctcagcaga 540  
 aaatcaacat gttcaacacc 560

<210> 42  
 <211> 186  
 <212> PRT  
 <213> Mycosphaerella graminicola

<400> 42

Leu Pro Ser Lys Arg Ala Gly Lys Glu Ala Gly Gly Trp Pro Glu Asp  
 1 5 10 15

Val Val Gly Pro Ser Gly Gly Glu Asp Phe Thr Trp Asp Glu Arg Ser  
 20 25 30

Ser Ser Asp Pro Ser Gly Gly Tyr Tyr Ala Pro Arg Glu Leu Ser Val  
 35 40 45

Arg Glu Ile Lys Glu Met Val Gln Asp Trp Ala Thr Ala Ala Lys Arg  
 50 55 60

Ala Val Lys Ala Gly Val Asp Val Ile Glu Ile His Gly Ala His Gly  
 65 70 75 80

Tyr Leu Ile His Glu Phe Leu Ser Pro Ile Thr Asn Arg Arg Thr Asp  
 85 90 95

Ser Tyr Gly Gly Ser Phe Glu Asn Arg Thr Arg Leu Leu Ile Glu Ile  
 100 105 110

Val Thr Ala Val Arg Ala Ala Met Pro Ser Ser Met Pro Leu Phe Leu  
 115 120 125

Arg Leu Ser Ser Thr Glu Trp Met Glu Asp Thr Asp Ile Gly Lys Lys  
 130 135 140

Phe Gly Ser Trp Asp Val Glu Ser Thr Ile Lys Ile Ser Lys Ile Leu  
 145 150 155 160

Ala Asp Leu Gly Val Asp Leu Leu Asp Val Ser Ser Gly Gly Asn His  
 165 170 175

Pro Gln Gln Lys Ile Asn Met Phe Asn Thr  
 180 185

P03371US0 Sequence listing).txt

<210> 43  
 <211> 1254  
 <212> DNA  
 <213> Magnaporthe grisea

<400> 43  
 atgtccccac cacgcttcga agcggcccct gccgaccctt caccgctcgg cacgccgctc 60  
 aaataccccg tctcggggcg gtcggcgccc aaccggttcc tcaacgcggc catgtcggag 120  
 ggcctggcga cgtttgacga ggcggaccgg tccaagcgcg gcatcccgac ggagcagctg 180  
 gtgcagctgt accggcgctg gggccagggc gagtggggcc agatccagac gggcaacgtc 240  
 atgatcgacc cggagcacct cgaggccccg ggcaacatgg tggcgccg cgacgccgag 300  
 ccctcggggc agcgttcga catgttttcc aagctcgccg ccgccgcaa ggagcacggc 360  
 agcctcatcg tcgcgcaggt cggacacccc ggtcgccagg cccgcggcag cgtccagcag 420  
 caccattta gcgccagcga cgtgcagctt aagcaggaga tgtttgggtc aaagtttggc 480  
 gtgcccaggc ccgctacaa ggaggatatt aaggcggtga ttgagggttt tgcccacacg 540  
 gccgagtacc ttgaaaaggc cggtttcgac ggtatcgaat tgcacgccgc ccacggttac 600  
 ctgctggccc aattcctgtc cgaaacaacc aaccagcgca ccgacgagta cggcggcagc 660  
 ctcgaaaacc gcatgcggct aatcctcgag gtcacggccg aggtccgcag gcggacgagc 720  
 aagaatttca tcctcggcat caaaattaac agcgtcgagt tccaggagaa gggtttcaag 780  
 ccagaggagg cgggtgcagtt gtgcgaggcc ctcgaggccg cgggcatgga ttttgtcgag 840  
 acgagcgggc gcacctatga gagttttggt tttgcgacc gcaaggagtc cagccgcaag 900  
 cgggagaact attttatcga gttcgccgag gtcacccgca aggccgtcaa gcacatggtg 960  
 gtctacacca ccggcggctt caagacggtg ggcgccatgg tcgacgcgct gcagggcgctc 1020  
 gatgggatag gcatcgggcg cgcagccggt tcggagccgg acctcgcaa ggacatcatc 1080  
 gcgggcaagg tgtccagcat tatcaaatac gccatggggg aggacgagtt tgtgctgcag 1140  
 ttgactgcct gctcggcgca aataaggctg atggccaagg gcgaggagcc gtttgacatc 1200  
 tcaaacgccg acgaggtggc gcgggtgacg cagttgatgg cggagggcaa ggtg 1254

<210> 44  
 <211> 418  
 <212> PRT  
 <213> Magnaporthe grisea

<400> 44  
 Met Ser Pro Pro Arg Phe Glu Ala Ala Pro Ala Asp Pro Ser Pro Leu  
 1 5 10 15  
 Gly Thr Pro Leu Lys Tyr Pro Val Ser Gly Arg Ser Ala Pro Asn Arg  
 20 25 30

P03371US0 Sequence listing).txt

Phe Leu Asn Ala Ala Met Ser Glu Gly Leu Ala Thr Phe Asp Glu Ala  
 35 40 45  
 Asp Pro Ser Lys Arg Gly Ile Pro Thr Glu Gln Leu Val Gln Leu Tyr  
 50 55 60  
 Arg Arg Trp Gly Gln Gly Glu Trp Gly Gln Ile Gln Thr Gly Asn Val  
 65 70 75 80  
 Met Ile Asp Pro Glu His Leu Glu Ala Pro Gly Asn Met Val Val Pro  
 85 90 95  
 Arg Asp Ala Glu Pro Ser Gly Glu Arg Phe Asp Met Phe Ser Lys Leu  
 100 105 110  
 Ala Ala Ala Ala Lys Glu His Gly Ser Leu Ile Val Ala Gln Val Gly  
 115 120 125  
 His Pro Gly Arg Gln Ala Arg Gly Ser Val Gln Gln His Pro Ile Ser  
 130 135 140  
 Ala Ser Asp Val Gln Leu Lys Gln Glu Met Phe Gly Ser Lys Phe Gly  
 145 150 155 160  
 Val Pro Arg Pro Ala Thr Lys Glu Asp Ile Lys Ala Val Ile Glu Gly  
 165 170 175  
 Phe Ala His Thr Ala Glu Tyr Leu Glu Lys Ala Gly Phe Asp Gly Ile  
 180 185 190  
 Glu Leu His Ala Ala His Gly Tyr Leu Leu Ala Gln Phe Leu Ser Glu  
 195 200 205  
 Thr Thr Asn Gln Arg Thr Asp Glu Tyr Gly Gly Ser Leu Glu Asn Arg  
 210 215 220  
 Met Arg Leu Ile Leu Glu Val Thr Ala Glu Val Arg Arg Arg Thr Ser  
 225 230 235 240  
 Lys Asn Phe Ile Leu Gly Ile Lys Ile Asn Ser Val Glu Phe Gln Glu  
 245 250 255  
 Lys Gly Phe Lys Pro Glu Glu Ala Val Gln Leu Cys Glu Ala Leu Glu  
 260 265 270  
 Ala Ala Gly Met Asp Phe Val Glu Thr Ser Gly Gly Thr Tyr Glu Ser  
 275 280 285

P03371US0 Sequence listing).txt

Phe Gly Phe Ala His Arg Lys Glu Ser Ser Arg Lys Arg Glu Asn Tyr  
290 295 300

Phe Ile Glu Phe Ala Glu Val Ile Arg Lys Ala Val Lys His Met Val  
305 310 315 320

Val Tyr Thr Thr Gly Gly Phe Lys Thr Val Gly Ala Met Val Asp Ala  
325 330 335

Leu Gln Gly Val Asp Gly Ile Gly Ile Gly Arg Ala Ala Gly Ser Glu  
340 345 350

Pro Asp Leu Ala Lys Asp Ile Ile Ala Gly Lys Val Ser Ser Ile Ile  
355 360 365

Lys Tyr Ala Met Gly Glu Asp Glu Phe Val Leu Gln Leu Thr Ala Cys  
370 375 380

Ser Ala Gln Ile Arg Leu Met Ala Lys Gly Glu Glu Pro Phe Asp Ile  
385 390 395 400

Ser Asn Ala Asp Glu Val Ala Arg Val Thr Gln Leu Met Ala Glu Gly  
405 410 415

Lys Val

<210> 45  
<211> 690  
<212> DNA  
<213> Aspergillus fumigatus

<400> 45  
agcttagacc tacagagagc attgctactg taagttgtat ttcgccttct cgcatagaac 60  
aaaatataac tgatggtgta ggtataaaac tagcatcctc ttccaccttt cagatccccc 120  
tgacaagcac cttatggctt tcgatggaaa cagctattcc ttctactggt aaaaatagga 180  
taccagaggc tacaatcaat acaccctcga tagaggctgt cgaatgtggc caactggcaa 240  
cgctgcgggt agtcatcgtc ggagactttc tgggattcat tttcttccga gtctccgcct 300  
gcttattaag gcatcaatct ggatgctcca ctgtggtaca tccaattttc gatttttctt 360  
cggcagaggc aaggattcca ctgggttcagt ctaggcattt agaagatcaa agctgtcctg 420  
tacctccgta cctgggtggt cgacgtcatt gccacgtttc gacccaaggg cagacgcat 480  
gtcgccgagc gatcgccgag atatgcctcg aatttgccg attcggcatc cagtttccag 540  
tgcccttccc cgaatgactg tctccactat tcggcaagat tgtaaataca gcctgaagaa 600

P03371US0 Sequence listing).txt

gcggagcatt cttggaagtc gtatgttcta ctgattctgt gcctggcgca gacgggtata 660  
taataaagat cacgcaccga ggagttctta 690

<210> 46  
<211> 19  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer

<400> 46  
gttcgacgtc attgccacg 19

<210> 47  
<211> 19  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 47  
ccttgatcgt tgctgagcg 19

<210> 48  
<211> 19  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 48  
atgactgtcg ccgatatcg 19

<210> 49  
<211> 22  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 49  
ctatacatcg aaaatagact gc 22

<210> 50  
<211> 26  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 50

P03371US0 Sequence listing).txt

ccgtcctggg cggagtattg gcagag 26

<210> 51  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 51  
 gcgaatcaga ttctagagga gcaggatattc g 31

<210> 52  
 <211> 27  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 52  
 gctcagcacc tcggcgtcga aatctcc 27

<210> 53  
 <211> 17  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 53  
 tctgccaata ctccgcc 17

<210> 54  
 <211> 16  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 54  
 ctttcgggcc ggcattg 16

<210> 55  
 <211> 35  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer

<400> 55  
 ggtattgagg gtcgcatgac tgtcgccgat atcga 35

P03371US0 Sequence listing).txt

<210> 56  
 <211> 45  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 56  
 agaggagagt tagagcctac atcgaaaata gactgcttgt acacc 45  
  
 <210> 57  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 57  
 ggtattgagg gtcgcatgtc gcaacctgtt gtg 33  
  
 <210> 58  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 58  
 agaggagagt tagagcctat atcttctcga gtttcttcc 39  
  
 <210> 59  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 59  
 ggtattgagg gtcgcatggg ttccaacgcc ttc 33  
  
 <210> 60  
 <211> 37  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 60  
 agaggagagt tagagcctaa atggccctgc caaactg 37  
  
 <210> 61  
 <211> 37  
 <212> DNA

P03371US0 Sequence listing).txt

<213> Artificial sequence

<220>

<223> primer

<400> 61  
ggtattgagg gtcgcatggc tctccctgac gtcgaaa 37

<210> 62  
<211> 35  
<212> DNA  
<213> Artificial sequence

<220>

<223> primer

<400> 62  
agaggagagt tagagcctac tcaaagatgc tctcc 35

<210> 63  
<211> 34  
<212> DNA  
<213> Artificial sequence

<220>

<223> primer

<400> 63  
ggtattgagg gtcgcatgac agttccatac caag 34

<210> 64  
<211> 42  
<212> DNA  
<213> Artificial sequence

<220>

<223> primer

<400> 64  
agaggagagt tagagcctaa tttacttcta atttagatgt tc 42

<210> 65  
<211> 33  
<212> DNA  
<213> Artificial sequence

<220>

<223> primer

<400> 65  
ggtattgagg gtcgcatgtc ggcagaaaag aag 33

<210> 66  
<211> 39  
<212> DNA  
<213> Artificial sequence

<220>

P03371US0 Sequence listing).txt

<223> primer

<400> 66  
agaggagagt tagagcccaa atccttgac ccttgcgcc 39

<210> 67  
<211> 19  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 67  
cagaccaatg gccagaaga 19

<210> 68  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 68  
agatgggcga tgtggtagtc 20

<210> 69  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 69  
gccgcttaca gggaatgata 20

<210> 70  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 70  
atggctcaat ctgcgagtct 20

<210> 71  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> primer

<400> 71

	P03371US0 Sequence listing).txt	
cgactcttgt gggtgctgta		20
<210> 72		
<211> 20		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> primer		
<400> 72		
gtggaaaaca cccattctgg		20
<210> 73		
<211> 20		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> primer		
<400> 73		
ccccaatcgt cagatgaagt		20
<210> 74		
<211> 20		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> primer		
<400> 74		
ctggcccacg attcactaat		20
<210> 75		
<211> 20		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> primer		
<400> 75		
caaaagatcg ccatccaact		20
<210> 76		
<211> 20		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> primer		
<400> 76		
ctggtgacga gtccctcaat		20

P03371US0 Sequence listing).txt

<210> 77  
 <211> 22  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 77  
 ccagcagatg ttcgacccca ag 22  
  
 <210> 78  
 <211> 24  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 78  
 cagtgaactc catctcgtcc atac 24  
  
 <210> 79  
 <211> 18  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 79  
 tccgtggcgt caccttcc 18  
  
 <210> 80  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> primer  
  
 <400> 80  
 cagatgggcg atgtggtagt c 21  
  
 <210> 81  
 <211> 5387  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> plasmid pZVK2  
  
 <400> 81  
 tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60  
 cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120  
 ttggcggggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180

P03371US0 Sequence listing).txt

accatatgcg gtgtgaaata ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc	240
attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat	300
tacgacagct gtctcttata cacatctcaa ccatcatcga tgaattttct cgggtgttct	360
cgcattattgg ctcgaattcg agctcgggtac ccggggatcc tctagaagtc ctgaatagta	420
gtttgtggat taacattggt ccgatgtagg aatcatgatc ccaaccagaa gagctggaca	480
gccccctcttc cagagcattt ttggtgggat gttttggctt agtgcgatgc aactggacaa	540
agtccttccg tttctactgc gtcttacatc atctggtatc tacgcaagcc gccacttac	600
catatgaata agaggcactc aggttttccc tcaccccccc gaagcgatgg taagcgggtg	660
ccaaatgcat cgggagtttc tctatcataa taacctaggt attccgtaat ctattaccag	720
tctttccgaa gagctggtag caactgcacg agattttag gagcgagtac ccggctggac	780
gagcacgcag cacggctatt ggtcagcatg gtagctaccg aggggaggca ggccgcccaa	840
atatcgtgag tctcctgctt tgcccgggtgt atgaaaccgg aaaagctgct atagagcttc	900
tgggcggcgc atgtcgggaa accagcagca agctgaccca gaaagaccg tcctcaagcc	960
attaccgtac taatcaatta tttgtgtagc aacctggga agctgtagtg cataggctgg	1020
agcagctatt tggcctttag ccccgctctgt ccgcccgggtg tgcggtttcg actggcgcgc	1080
aagctcaagg tgatcaggtc gttgcgtcag tcggagacaa caagccattg ctttttctac	1140
tgccccctccc ccgctgggtgg cttttttctc tcattcttctc ctctcttccc atcatcagca	1200
tcattaatct actgtctctc tttctttcta tcattctata aagtaagaac atatccatct	1260
tccctcaatc ccgtctacaa tagtgtctc ttactactc tgtctctatc tctcaaagct	1320
tgactgacat ttaccccgtc cagtaccaga cgaatctaca cagaattcga gctcactaaa	1380
ccatggccaa gttgaccagt gccgttccgg tgctcaccgc gcgcgacgtc gccggagcgg	1440
tcgagttctg gaccgaccgg ctcgggttct cccgggactt cgtggaggac gacttcgccg	1500
gtgtggtccg ggacgacgtg accctgttca tcagcgcggt ccaggaccag gtggtgccgg	1560
acaacaccct ggcctgggtg tgggtgcgcg gcctggacga gctgtacgcc gagtggctcg	1620
aggtcgtgtc cacgaacttc cgggacgcct ccgggccggc catgaccgag atcggcgagc	1680
agccgtgggg gcgggagttc gccctgcgcg acccgccgg caactgcgtg cacttcgtgg	1740
ccgaggagca ggactgagaa ttccactagt gcagaaagct gttttccttg ctctgtggta	1800
taagtctagt gccactattc tatgatgagt tgatgactct ttcattgactg gaaggcttac	1860
atttccaag atcatgtctc actcaaaact tatctcgggt tcactttcgg gttccatata	1920
tctcatcatt tctgggttta gaaacatctc tctcgttttt gcagctcttc tacgtactcc	1980
tagcggtttc actgaaatga atacatttgg gtaacctaat tgccaattca tatcttcctg	2040
agggcagtaa cacatcacgt acattctatc agctgtgata gagttacaaa actagcaata	2100

P03371US0 Sequence listing).txt

cttttatgct	tcctcctttc	ttaccattta	cacatccgct	ttctctctgc	tcttgatctt	2160
ggccccctgat	tgtattgtca	cctcaccaaa	ttcaagtcac	cacctcttct	ctagagtcga	2220
cttttatgga	cagcaagcga	accggaattg	ccagctgggg	cgccctctgg	taagggtggg	2280
aagccctgca	aagtaaactg	gatggctttc	tcgccgcaa	ggatctgatg	gcgcagggga	2340
tcaagctctg	atcaagagac	aggatgagga	tcgtttcgca	tgattgaaca	agatggattg	2400
cacgcagggt	ctccggccgc	ttgggtggag	aggctattcg	gctatgactg	ggcacaacag	2460
acaatcggct	gctctgatgc	cgccgtgttc	cggtgtcag	cgcaggggcg	cccggttctt	2520
tttgtcaaga	ccgacctgtc	cggtgccctg	aatgaactgc	aagacgaggc	agcgcggcta	2580
tcgtggctgg	ccacgacggg	cgttccttgc	gcagctgtgc	tcgacgttgt	caactgaagcg	2640
ggaagggact	ggctgctatt	gggcgaagtg	ccggggcagg	atctcctgtc	atctcacctt	2700
gctcctgccg	agaaagtatc	catcatggct	gatgcaatgc	ggcggctgca	tacgcttgat	2760
ccggctacct	gcccattcga	ccaccaagcg	aaacatcgca	tcgagcgagc	acgtactcgg	2820
atggaagccg	gtcttgctga	tcaggatgat	ctggacgaag	agcatcaggg	gctcgcgcca	2880
gccgaactgt	tcgccaggct	caaggcgagc	atgcccgacg	gcgaggatct	cgctcgtgacc	2940
catggcgatg	cctgcttgcc	gaatatcatg	gtggaaaatg	gccgcttttc	tggattcatc	3000
gactgtggcc	ggctgggtgt	ggcggaccgc	tatcaggaca	tagcgttggc	taccctgat	3060
attgctgaag	agcttggcgg	cgaatgggct	gaccgcttcc	tcgtgcttta	cggtatcgcc	3120
gctcccgaatt	cgacgcgcac	cgccttctat	cgccttcttg	acgagttctt	ctgaattatt	3180
aacgcttaca	atttcctgat	gcggtatttt	ctcgcacgca	tcactagtga	attcgcggcc	3240
gcctgcagggt	cgacctgcag	gcatgcaagc	ttgccaacga	ctacgcacta	gccaacaaga	3300
gcttcagggt	tgagatgtgt	ataagagaca	gctgtcttaa	tgaatcggcc	aacgcgcggg	3360
gagaggcgggt	ttgcgtattg	ggcgcctctc	cgcttcctcg	ctcactgact	cgctgcgctc	3420
ggctcgttcg	ctgcggcgag	cggtatcagc	tcactcaaag	gcggtataac	ggttatccac	3480
agaatcagggt	gataacgcag	gaaagaacat	gtgagcaaaa	ggccagcaaa	aggccaggaa	3540
ccgtaaaaag	gccgcgttgc	tggcgttttt	ccataggctc	cgccccctg	acgagcatca	3600
caaaaatcga	cgctcaagtc	agaggtggcg	aaacccgaca	ggactataaa	gataaccaggc	3660
gtttccccct	ggaagctccc	tcgtgcgctc	tcctgttccg	accctgccgc	ttaccggata	3720
cctgtccgcc	tttctccctt	cggaagcgt	ggcgccttct	catagctcac	gctgtaggta	3780
tctcagttcg	gtgtaggtcg	ttcgctccaa	gctgggctgt	gtgcacgaac	cccccgttca	3840
gcccgaccgc	tgcgcttat	ccggtacta	tcgtcttgag	tccaacccgg	taagacacga	3900
cttatcgcca	ctggcagcag	ccactggtaa	caggattagc	agagcgagggt	atgtaggcgg	3960

P03371US0 Sequence listing).txt

tgctacagag ttcttgaagt ggtggcctaa ctacggctac actagaagga cagtatttgg	4020
tatctgcgct ctgctgaagc cagttacctt cggaanaaga gttggtagct cttgatccgg	4080
caaacaaacc accgctggta gcggtggttt ttttgtttgc aagcagcaga ttacgcgcag	4140
aaaaaaagga tctcaagaag atcctttgat cttttctacg gggctctgacg ctcagtggaa	4200
cgaaaactca cgtaagggga ttttggtcat gagattatca aaaaggatct tcacctagat	4260
ccttttaaat taaaaatgaa gttttaaatc aatctaaagt atatatgagt aaacttggtc	4320
tgacagttac caatgcttaa tcagtgaggc acctatctca gcgatctgtc tatttcgttc	4380
atccatagtt gcctgactcc ccgtcgtgta gataactacg atacgggagg gcttaccatc	4440
tggccccagt gctgcaatga taccgcgaga cccacgctca ccggctccag atttatcagc	4500
aataaaccag ccagccggaa gggccgagcg cagaagtggc cctgcaactt tatccgcctc	4560
catccagtct attaatgttt gccgggaagc tagagtaagt agttcgccag ttaatagttt	4620
gcgcaacggt gttgccattg ctacaggcat cgtggtgtca cgctcgtcgt ttggtatggc	4680
ttcattcagc tccggttccc aacgatcaag gcgagttaca tgatcccca tgttgtgcaa	4740
aaaagcggtt agctccttcg gtcctccgat cgttgtcaga agtaagttgg ccgcagtgtt	4800
atcactcatg gttatggcag cactgcataa ttctcttact gtcatgccat ccgtaagatg	4860
cttttctgtg actggtgagt actcaaccaa gtcattctga gaatagtgtg tgcggcgacc	4920
gagttgctct tgcccggcgt caatacggga taataccgcg ccacatagca gaactttaaa	4980
agtgtctatc attggaanaac gttcttcggg gcgaaaactc tcaaggatct taccgctgtt	5040
gagatccagt tcgatgtaac cactcgtgc acccaactga tcttcagcat cttttacttt	5100
caccagcggt tctgggtgag caaaaacagg aaggcaaat gccgcaaaa aggggaataag	5160
ggcgacacgg aaatgttgaa tactcatact ctctcttttt caatattatt gaagcattta	5220
tcagggttat tgtctcatga gcggatacat atttgaatgt atttagaaaa ataaacaaat	5280
aggggttccg cgcacatttc cccgaaaagt gccacctgac gtctaagaaa ccattattat	5340
catgacatta acctataaaa ataggcgtat cacgaggccc tttcgtc	5387

<210> 82  
 <211> 1326  
 <212> DNA  
 <213> Fusarium graminearum

<400> 82	
atgacagttc aatcacagca acaatcccag gctattcccg tcctttcttc ccagaatggc	60
actgaacccc aagacgcaa caaggagggt gttcagaatg tcgctgccaa aggagtgcaa	120
tacttcaacc ctgagcaact tcctgcacca ggtctcggtg taaacgggtc caataatact	180
ctaccaaagg tctttacacc catcaagatt cgcggcatga ccatgcccaa ccgtatctgg	240

P05371.050 Sequence (1318197).txt						
gtcagcccca	tgtgcccaata	cagtgcccg	gacggccttc	agcagccttg	gcactttgcc	300
cactacggcg	gactggccca	acgtggccct	ggcctcatca	tgctagaagc	taccgcagtt	360
caagcacgtg	gccgtatcac	acctgaagat	tctggcatct	ggctagactc	tcattgttgag	420
ggactgcgaa	agcacgtcga	gtttgcccac	gccacaact	ctcttatcgg	tatccagatt	480
ggccatgctg	gtcgcaaggc	ctcctgcgtt	gtccttggt	tagacgccgg	acttgccgct	540
gaaaaggccg	ctggtggatg	gcccgatgac	gttgctggac	ctagcaacga	gccttttgct	600
cctggctacc	ctaccccccg	tgctattact	cttgaagaga	ttgaacagtt	gaaggaggac	660
tttgtttccg	gtgttcgtcg	agcggttgaa	gcaggatttg	acactatcga	cttccatttc	720
gctcacggtt	atcttgtttc	cagcttcctg	tcccctgcc	ccaacaagcg	taccgacaag	780
tacggaggta	gcttcgagaa	cagagtgcgc	cttgctctcg	agattgtcga	ggctgcacga	840
gctgttatgc	ctgaggacat	gcccttgttc	actcgcatca	gtggaactga	ctggctggag	900
aacaaccctg	agtacgaggg	agagacctgg	actcttgagc	agagcatcaa	gcttgcacac	960
cagttagcag	accgtggtgt	cgatgttttg	gatgtttcca	gtggtggcat	ccacaagatg	1020
caaaaggctg	ctgctggtcc	cggttaccag	gcacctcttg	ccaaggcgat	caagaagtca	1080
gttgagagaca	agatgttgat	cagcactggt	ggtagcatca	agataggtac	ccttgcgag	1140
gagatcatcg	ctggaggaga	ggacgatacc	cccttggatc	ttgtggcttc	aggccgtctg	1200
ttccagaaga	acactggact	tgtttggtca	tgggctgacg	atctgaacac	ttctatccag	1260
atcgctcatc	agatcgcatg	gggtttcggt	ggcagagcta	agaagaacgc	tccaagctt	1320
gtctta						1326

```
<210> 83
<211> 442
<212> PRT
<213> Fusarium graminearum
```

<400> 83

Met Thr Val Gln Ser Gln Gln Gln Ser Gln Ala Ile Pro Val Leu Ser  
1 5 10 15

Ser Gln Asn Gly Thr Glu Pro Gln Asp Ala Asn Lys Glu Val Val Gln  
20 25 30

Asn Val Ala Ala Lys Gly Val Gln Tyr Phe Asn Pro Glu Gln Leu Pro  
35 40 45

Ala Pro Gly Leu Gly Ile Asn Gly Pro Asn Asn Thr Leu Pro Lys Val  
50 55 60

Phe Thr Pro Ile Lys Ile Arg Gly Met Thr Met Pro Asn Arg Ile Trp  
Page 57

```

65              70              75              80
Val Ser Pro Met Cys Gln Tyr Ser Ala Arg Asp Gly Phe Gln Gln Pro
            85              90              95

Trp His Phe Ala His Tyr Gly Gly Leu Ala Gln Arg Gly Pro Gly Leu
            100              105              110

Ile Met Leu Glu Ala Thr Ala Val Gln Ala Arg Gly Arg Ile Thr Pro
            115              120              125

Glu Asp Ser Gly Ile Trp Leu Asp Ser His Val Glu Gly Leu Arg Lys
            130              135              140

His Val Glu Phe Ala His Ala Asn Asn Ser Leu Ile Gly Ile Gln Ile
            145              150              155              160

Gly His Ala Gly Arg Lys Ala Ser Cys Val Ala Pro Trp Leu Asp Ala
            165              170              175

Gly Leu Ala Ala Glu Lys Ala Ala Gly Gly Trp Pro Asp Asp Val Val
            180              185              190

Gly Pro Ser Asn Glu Pro Phe Ala Pro Gly Tyr Pro Thr Pro Arg Ala
            195              200              205

Ile Thr Leu Glu Glu Ile Glu Gln Leu Lys Glu Asp Phe Val Ser Gly
            210              215              220

Val Arg Arg Ala Val Glu Ala Gly Phe Asp Thr Ile Asp Phe His Phe
            225              230              235              240

Ala His Gly Tyr Leu Val Ser Ser Phe Leu Ser Pro Ala Thr Asn Lys
            245              250              255

Arg Thr Asp Lys Tyr Gly Gly Ser Phe Glu Asn Arg Val Arg Leu Ala
            260              265              270

Leu Glu Ile Val Glu Ala Ala Arg Ala Val Met Pro Glu Asp Met Pro
            275              280              285

Leu Phe Thr Arg Ile Ser Gly Thr Asp Trp Leu Glu Asn Asn Pro Glu
            290              295              300

Tyr Glu Gly Glu Thr Trp Thr Leu Glu Gln Ser Ile Lys Leu Ala His
            305              310              315              320

```

P03371US0 Sequence listing).txt

Gln Leu Ala Asp Arg Gly Val Asp Val Leu Asp Val Ser Ser Gly Gly  
325 330 335

Ile His Lys Met Gln Lys Val Ala Ala Gly Pro Gly Tyr Gln Ala Pro  
340 345 350

Leu Ala Lys Ala Ile Lys Lys Ser Val Gly Asp Lys Met Leu Ile Ser  
355 360 365

Thr Val Gly Ser Ile Lys Ile Gly Thr Leu Ala Glu Glu Ile Ile Ala  
370 375 380

Gly Gly Glu Asp Asp Thr Pro Leu Asp Leu Val Ala Ser Gly Arg Leu  
385 390 395 400

Phe Gln Lys Asn Thr Gly Leu Val Trp Ser Trp Ala Asp Asp Leu Asn  
405 410 415

Thr Ser Ile Gln Ile Ala His Gln Ile Ala Trp Gly Phe Gly Gly Arg  
420 425 430

Ala Lys Lys Asn Ala Pro Lys Leu Val Leu  
435 440

<210> 84  
<211> 1350  
<212> DNA  
<213> Ustilago maydis

<400> 84  
atggacacgt ctcgattcgt gtctggtctc acaccgcctc tcgtcgactc gatcgatgca 60  
ctcaagatca gcaactttgt cccactcga agtggccacc ctctctctgg ctcggtcccg 120  
gaatccatcc tgccagaggg tgtcaaaaaa ccggctttgt tccaaacgtt gacattgccc 180  
tttgctgcac cggaacaggc gggtaagatg accttcaaga accgcatcat tgtctctccc 240  
atgtgccagt actctgcgaa caatggtctt cctactccgt accacattgc gcatttgggg 300  
tcgtttgccc tgcacggtgt gggaaacgtc atggtcgaag catctggtgt tgagccagag 360  
gggaggatca cgcctcagga cctgggtatt tggtcggaac agcatcggga tgcacacaag 420  
gcgctggtgt cggtgctcaa gtccttcacg gatggtctgg gtgtagggct gcaactggcg 480  
catgcgggaa ggaaggcctc ggactggtca ctttctacc gcggagaaaa gaagcaaaag 540  
tttgtgacgc aggaggaagg tggctggccg gatcgtgtcg tcgctccttc ggccatcgca 600  
tatgcgcaag gtcacgttac ccctcgagct ctcacgaccg aggacatcaa caagttgcaa 660  
gacaaattcg ttcagtcggc acgatgggcg tttgaagctg ggtatgacta cgtcgaactt 720  
cacagcgctc acggatacct gatgcactcg ttctcagcc cgttgaccaa tcagcgatcc 780

P03371U50 Sequence listing).txt

```

gacgagtacg gcggtagcct ggagaaccgc gctcgatttc tgctcaacgt tgcccgtcga      840
atccgccaag aattcccca caaggggtctc tgggtgcgcg tcagctccac cgactgggcc      900
gaccaagcgc accaagccga ctcttgacc gttgaccaga cggttgaact cgccaagatg      960
ctccaagagg ctcgagtcga cctgctagac gtcagctccg gcggcctggt tccattccaa     1020
aaaatcaccg tgggagccgg ataccagcta ttcggagcaa aagccgttcg cgatgctctg     1080
gccaaaatcg aaccgcagcg gtccaaacgc atgctcgctg gggccgtggg aatgatggaa     1140
ggttcctacg attcgcccaa cggccaagac cgcagccaga ttggcaagtt ggccgagcag     1200
tcgattcaga gcggagagtg tgatgcggtg ctgttggcac gtggattgat gtcctacca     1260
agctggaccg aggatgctag tgtagcgctg atgggtacca gggcagctgg caaccgcag      1320
taccatcgcg ttcacgtggc taagaagtga      1350

```

```

<210> 85
<211> 449
<212> PRT
<213> Ustilago maydis
<400> 85

```

```

Met Asp Thr Ser Arg Phe Val Ser Gly Leu Thr Pro Pro Leu Val Asp
1          5          10          15

```

```

Ser Ile Asp Ala Leu Lys Ile Ser Asn Phe Val Pro Thr Arg Ser Gly
          20          25          30

```

```

His Pro Pro Pro Gly Ser Val Pro Glu Ser Ile Leu Pro Glu Gly Val
          35          40          45

```

```

Lys Lys Pro Ala Leu Phe Gln Thr Leu Thr Leu Pro Phe Ala Ala Pro
          50          55          60

```

```

Glu Gln Ala Gly Lys Met Thr Phe Lys Asn Arg Ile Ile Val Ser Pro
65          70          75          80

```

```

Met Cys Gln Tyr Ser Ala Asn Asn Gly Leu Pro Thr Pro Tyr His Ile
          85          90          95

```

```

Ala His Leu Gly Ser Phe Ala Leu His Gly Val Gly Asn Val Met Val
          100          105          110

```

```

Glu Ala Ser Gly Val Glu Pro Glu Gly Arg Ile Thr Pro Gln Asp Leu
          115          120          125

```

```

Gly Ile Trp Ser Glu Gln His Arg Asp Ala His Lys Ala Leu Val Ser
          130          135          140

```

P03371US0 Sequence listing).txt

Val Leu Lys Ser Phe Thr Asp Gly Leu Gly Val Gly Leu Gln Leu Ala  
145 150 155 160

His Ala Gly Arg Lys Ala Ser Asp Trp Ser Pro Phe Tyr Arg Gly Glu  
165 170 175

Lys Lys Gln Lys Phe Val Thr Gln Glu Glu Gly Gly Trp Pro Asp Arg  
180 185 190

Val Val Ala Pro Ser Ala Ile Ala Tyr Ala Gln Gly His Val Thr Pro  
195 200 205

Arg Ala Leu Thr Thr Glu Asp Ile Asn Lys Leu Gln Asp Lys Phe Val  
210 215 220

Gln Ser Ala Arg Trp Ala Phe Glu Ala Gly Tyr Asp Tyr Val Glu Leu  
225 230 235 240

His Ser Ala His Gly Tyr Leu Met His Ser Phe Leu Ser Pro Leu Thr  
245 250 255

Asn Gln Arg Thr Asp Glu Tyr Gly Gly Ser Leu Glu Asn Arg Ala Arg  
260 265 270

Phe Leu Leu Asn Val Ala Arg Arg Ile Arg Gln Glu Phe Pro Asn Lys  
275 280 285

Gly Leu Trp Val Arg Val Ser Ser Thr Asp Trp Ala Asp Gln Ala His  
290 295 300

Gln Ala Asp Ser Trp Thr Val Asp Gln Thr Val Glu Leu Ala Lys Met  
305 310 315 320

Leu Gln Glu Ala Arg Val Asp Leu Leu Asp Val Ser Ser Gly Gly Leu  
325 330 335

Val Pro Phe Gln Lys Ile Thr Val Gly Ala Gly Tyr Gln Leu Phe Gly  
340 345 350

Ala Lys Ala Val Arg Asp Ala Leu Ala Lys Ile Glu Pro Asp Ala Ser  
355 360 365

Lys Arg Met Leu Val Gly Ala Val Gly Met Met Glu Gly Ser Tyr Asp  
370 375 380

Ser Pro Asn Gly Gln Asp Arg Ser Gln Ile Gly Lys Leu Ala Glu Gln

P03371US0 Sequence listing).txt

385 390 395 400

Ser Ile Gln Ser Gly Glu Cys Asp Ala Val Leu Leu Ala Arg Gly Leu  
405 410 415

Met Ser Tyr Pro Ser Trp Thr Glu Asp Ala Ser Val Ala Leu Met Gly  
420 425 430

Thr Arg Ala Ala Gly Asn Pro Gln Tyr His Arg Val His Val Ala Lys  
435 440 445

Lys

<210> 86  
<211> 363  
<212> PRT  
<213> Pseudomonas putida

<400> 86

Met Ser Ala Leu Phe Glu Pro Tyr Thr Leu Lys Asp Val Thr Leu Arg  
1 5 10 15

Asn Arg Ile Ala Ile Pro Pro Met Cys Gln Tyr Met Ala Glu Asp Gly  
20 25 30

Leu Ile Asn Asp Trp His Gln Val His Tyr Ala Ser Met Ala Arg Gly  
35 40 45

Gly Ala Gly Leu Leu Val Val Glu Ala Thr Ala Val Ala Pro Glu Gly  
50 55 60

Arg Ile Thr Pro Gly Cys Ala Gly Ile Trp Ser Asp Ala His Ala Gln  
65 70 75 80

Ala Phe Val Pro Val Val Gln Ala Ile Lys Ala Ala Gly Ser Val Pro  
85 90 95

Gly Ile Gln Ile Ala His Ala Gly Arg Lys Ala Ser Ala Asn Arg Pro  
100 105 110

Trp Glu Gly Asp Asp His Ile Gly Ala Asp Asp Ala Arg Gly Trp Glu  
115 120 125

Thr Ile Ala Pro Ser Ala Ile Ala Phe Gly Ala His Leu Pro Asn Val  
130 135 140

Pro Arg Ala Met Thr Leu Asp Asp Ile Ala Arg Val Lys Gln Asp Phe  
Page 62

P03371US0 Sequence listing).txt

145 150 155 160

Val Asp Ala Ala Arg Arg Ala Arg Asp Ala Gly Phe Glu Trp Ile Glu  
165 170 175

Leu His Phe Ala His Gly Tyr Leu Gly Gln Ser Phe Phe Ser Glu His  
180 185 190

Ser Asn Lys Arg Thr Asp Ala Tyr Gly Gly Ser Phe Asp Asn Arg Ser  
195 200 205

Arg Phe Leu Leu Glu Thr Leu Ala Ala Val Arg Glu Val Trp Pro Glu  
210 215 220

Asn Leu Pro Leu Thr Ala Arg Phe Gly Val Leu Glu Tyr Asp Gly Arg  
225 230 235 240

Asp Glu Gln Thr Leu Glu Glu Ser Ile Glu Leu Ala Arg Arg Phe Lys  
245 250 255

Ala Gly Gly Leu Asp Leu Leu Ser Val Ser Val Gly Phe Thr Ile Pro  
260 265 270

Glu Thr Asn Ile Pro Trp Gly Pro Ala Phe Met Gly Pro Ile Ala Glu  
275 280 285

Arg Val Arg Arg Glu Ala Lys Leu Pro Val Thr Ser Ala Trp Gly Phe  
290 295 300

Gly Thr Pro Gln Leu Ala Glu Ala Ala Leu Gln Ala Asn Gln Leu Asp  
305 310 315 320

Leu Val Ser Val Gly Arg Ala His Leu Ala Asp Pro His Trp Ala Tyr  
325 330 335

Phe Ala Ala Lys Glu Leu Gly Val Glu Lys Ala Ser Trp Thr Leu Pro  
340 345 350

Ala Pro Tyr Ala His Trp Leu Glu Arg Tyr Arg  
355 360

<210> 87  
<211> 359  
<212> PRT  
<213> Streptomyces coelicolor  
  
<400> 87

Met Ser Ala Leu Phe Glu Pro Phe Arg Leu Arg Asp Thr Thr Ile Pro  
Page 63

P03371US0 Sequence listing).txt

1	5	10	15
Asn	Arg	Ile	Trp
20	Met	Pro	Pro
Met	Cys	Gln	Tyr
25	Ser	Ala	Ala
30	Pro	Glu	
Gly	Pro	Ser	Ala
35	Gly	Val	Pro
40	Gly	Asp	Trp
45	His	Phe	Ala
50	His	Tyr	Gly
Ala	Arg	Ala	Val
55	Gly	Gly	Thr
60	Gly	Leu	Ile
65	Val	Val	Glu
70	Ala	Thr	Gly
75	Val	Ser	Pro
80	Glu	Gly	Leu
85	Trp	Asn	
90	Asp	Leu	Gly
95	Leu	Trp	Asn
100	Val	Ser	Pro
105	Glu	Gly	Arg
110	Ile	Ser	Pro
115	Gln	Asp	Leu
120	Gly	Leu	Trp
125	Ala	His	Ala
130	Gly	Arg	Lys
135	Ala	Asp	Ala
140	Ala	Val	Gly
145	Ala	Pro	Val
150	Gly	Ala	Pro
155	Gly	Ala	Pro
160	Gly	Ala	Pro
165	Gly	Ala	Pro
170	Gly	Ala	Pro
175	Gly	Ala	Pro
180	Gly	Ala	Pro
185	Gly	Ala	Pro
190	Gly	Ala	Pro
195	Gly	Ala	Pro
200	Gly	Ala	Pro
205	Gly	Ala	Pro
210	Gly	Ala	Pro
215	Gly	Ala	Pro
220	Gly	Ala	Pro
225	Gly	Ala	Pro
230	Gly	Ala	Pro
235	Gly	Ala	Pro
240	Gly	Ala	Pro
245	Gly	Ala	Pro
250	Gly	Ala	Pro
255	Gly	Ala	Pro

P03371US0 Sequence listing).txt

Asp Leu Glu Ala His Gly Ile Asp Leu Leu Asp Val Ser Thr Gly Gly  
260 265 270

Asn Val Pro Arg Val Arg Ile Pro Thr Gly Pro Gly Tyr Gln Val Pro  
275 280 285

Phe Ala Ala Arg Val Lys Ala Gly Ser Thr Leu Pro Val Ala Ala Val  
290 295 300

Gly Leu Ile Thr Glu Pro Gly Gln Ala Glu Lys Ile Leu Ala Asn Gly  
305 310 315 320

Glu Ala Asp Ala Val Leu Leu Gly Arg Glu Leu Leu Arg Asn Pro Ser  
325 330 335

Trp Ala Gln His Ala Ala Arg Glu Leu Gly Val Asp Ala Arg Met Pro  
340 345 350

Asp Gln Tyr Gly Trp Gly Met  
355

<210> 88  
<211> 370  
<212> PRT  
<213> Deinococcus radiodurans

<400> 88

Met Thr Val Ser Ser Ala Ala Ala Pro Gln Pro Ala Ser Pro Ala Ala  
1 5 10 15

Pro Leu Leu Phe Thr Pro Leu Lys Leu Arg Ser Leu Glu Leu Pro Asn  
20 25 30

Arg Val Val Val Ser Pro Met Cys Thr Tyr Ser Ala Thr Asp Gly Val  
35 40 45

Ala Asn Glu Phe His Leu Val His Leu Gly Gln Tyr Ala Leu Gly Gly  
50 55 60

Ala Gly Leu Ile Leu Ala Glu Ala Thr Ala Val Ser Pro Glu Gly Arg  
65 70 75 80

Ile Thr Pro Glu Asp Leu Gly Leu Trp Asp Asp Arg Gln Ile Val Pro  
85 90 95

Leu Gly His Ile Thr Asp Phe Val His Gln His Gly Gly His Ile Gly  
100 105 110

P03371US0 Sequence listing).txt

Val Gln Leu Ala His Ala Gly Arg Lys Ala Ser Thr Tyr Ala Pro Trp  
115 120 125

Arg Gly Lys Gly Ala Val Pro Ala Glu Leu Gly Gly Trp Gln Val Ile  
130 135 140

Gly Pro Asp Glu Asn Ser Phe His Asp Leu Phe Pro Thr Pro Ala Met  
145 150 155 160

Met Gly Ala Asp Glu Leu Arg Gly Val Val Asp Ala Phe Ser Ala Ala  
165 170 175

Ala Arg Arg Ala Gln Val Ala Gly Phe Asp Ala Val Glu Val His Ala  
180 185 190

Ala His Gly Tyr Leu Leu His Gln Phe Leu Ser Pro Leu Ala Asn Thr  
195 200 205

Arg Thr Asp Asp Tyr Gly Gly Ser Phe Glu Asn Arg Thr Arg Leu Leu  
210 215 220

Leu Glu Val Val Arg Ala Val Arg His Val Trp Pro Ala His Leu Pro  
225 230 235 240

Leu Phe Val Arg Leu Ser Ala Thr Asp Trp Ala Glu Gly Gly Trp Asp  
245 250 255

Leu Glu Gln Thr Val Gln Leu Ser Lys Leu Leu Lys Tyr Glu Gly Val  
260 265 270

Asp Val Leu Asp Ile Ser Ser Gly Gly Leu Thr Ala Ala Gln Gln Ile  
275 280 285

Glu Val Gly Pro Gly Tyr Gln Val Pro Phe Ala Ala Ala Val Ser Arg  
290 295 300

Ala Glu Thr Glu Ile Ser Val Met Ala Val Gly Leu Ile Glu Thr Gly  
305 310 315 320

Ala Gln Ala Glu Ala Ile Leu Gln Ala Gly Asp Ala Asp Leu Ile Ala  
325 330 335

Leu Gly Arg Pro Phe Leu Arg Asp Pro His Trp Ala Gln Arg Ala Ala  
340 345 350

Arg Glu Leu Gly Leu Arg Pro Val Ser Ile Asp Gln Tyr Ala Arg Ala  
355 360 365

P03371US0 Sequence listing).txt

Gly Trp  
370

<210> 89  
<211> 773  
<212> PRT  
<213> Azoarcus evansii

<400> 89

Met Arg Ile Val Cys Ile Gly Gly Gly Pro Ala Gly Leu Tyr Phe Ala  
1 5 10 15

Ile Leu Met Lys Lys Leu Asn Pro Ala His Glu Ile Arg Val Ile Glu  
20 25 30

Arg Asn Arg Pro Tyr Asp Thr Phe Gly Trp Gly Val Val Phe Ser Asp  
35 40 45

Ala Thr Met Asp Asn Met Arg Glu Trp Asp Ser Glu Thr Ala Asp Ala  
50 55 60

Ile Gln Val Ala Phe Asn His Trp Asp Asp Ile Glu Leu His Phe Lys  
65 70 75 80

Gly Arg Thr Ile Arg Ser Gly Gly His Gly Phe Val Gly Ile Gly Arg  
85 90 95

Lys Met Met Leu Asn Ile Leu Gln Ala Arg Cys Glu Glu Leu Gly Val  
100 105 110

Glu Leu Val Phe Asp Arg Glu Val Glu Ser Asp Ala Glu Phe Pro Asp  
115 120 125

Ala Asp Leu Val Ile Ala Ser Asp Gly Ile Asn Ser Arg Ile Arg Asn  
130 135 140

Lys Tyr Ala Glu Val Phe Lys Pro Asp Ile Val Thr Arg Pro Asn Arg  
145 150 155 160

Tyr Ile Trp Leu Gly Thr Thr Lys Leu Phe Asp Ala Phe Thr Phe Phe  
165 170 175

Phe Glu Lys Thr Glu His Gly Trp Phe Gln Ala His Ile Tyr Lys Phe  
180 185 190

Asp Asp Lys Thr Thr Thr Phe Ile Val Glu Cys Pro Glu His Val Trp  
195 200 205

P03371U50 Sequence listing).txt

Lys Ala His Gly Leu Asp Thr Ala Asp Gln Glu Gln Ser Ile Ala Phe  
210 215 220

Cys Glu Gln Leu Phe Gly Lys His Leu Asp Gly His Arg Leu Met Thr  
225 230 235 240

Asn Ser Arg His Leu Arg Gly Ser Ala Trp Leu Asn Phe Gln Arg Val  
245 250 255

Lys Cys Glu Gln Trp His His Tyr Asn Gly Lys Ser His Val Val Leu  
260 265 270

Met Gly Asp Ala Val His Thr Ala His Phe Ala Ile Gly Ser Gly Thr  
275 280 285

Lys Leu Ala Leu Glu Asp Ala Ile Glu Leu Thr Arg Leu Phe Arg Asp  
290 295 300

Glu Gly Asp Thr Arg Glu His Ile Pro Ala Val Leu Glu Arg Tyr Gln  
305 310 315 320

Ala Ala Arg Asn Ile Asp Val Leu Arg Leu Gln Asn Ala Ala Trp Asn  
325 330 335

Ala Met Glu Trp Phe Glu Val Cys Gly Ala Arg Tyr Cys Asp Thr Leu  
340 345 350

Glu Pro Glu Gln Phe Met Tyr Ser Met Leu Thr Arg Ser Gln Arg Ile  
355 360 365

Ser His Glu Asn Leu Arg Leu Arg Asp Ala Gly Trp Leu Glu Gly Tyr  
370 375 380

Glu Arg Trp Leu Ala Arg Lys Ala Gly Met Thr Val Arg Asp Asp Glu  
385 390 395 400

Thr Pro Pro Pro Pro Met Phe Thr Pro Phe Lys Leu Arg Gly Leu Thr  
405 410 415

Leu Ala Asn Arg Ile Val Met Ser Pro Met Ala Met Tyr Ser Ala Glu  
420 425 430

Asp Gly Ala Pro Thr Asp Phe His Leu Val His Phe Gly Ser Arg Ala  
435 440 445

Leu Gly Gly Ala Gly Leu Leu Tyr Thr Glu Met Thr Cys Val Ser Pro  
450 455 460

P03371US0 Sequence listing).txt

Asp Ala Arg Ile Thr Pro Gly Cys Ala Gly Met Tyr Lys Pro Glu His  
465 470 475 480

Val Asn Ala Trp Lys Arg Ile Val Asp Phe Val His Gly Asn Ser Asp  
485 490 495

Ala Lys Ile Gly Met Gln Leu Gly His Ala Gly Arg Lys Gly Ala Thr  
500 505 510

Lys Leu Ala Trp Glu Gly Ile Asp Glu Pro Leu Glu Ala Gly Ala Trp  
515 520 525

Glu Leu Ile Ser Ala Ser Pro Leu Pro Tyr Leu Pro His Ser Gln Val  
530 535 540

Pro Arg Ala Met Thr Arg Asp Asp Met Glu Arg Val Arg Asn Asp Phe  
545 550 555 560

Val Arg Ala Thr Arg Met Ala Ala Glu Ala Gly Phe Asp Ile Leu Glu  
565 570 575

Leu His Cys Ala His Gly Tyr Leu Leu Ser Ser Phe Leu Ser Pro Leu  
580 585 590

Thr Asn Arg Arg Thr Asp Glu Phe Gly Gly Asp Leu Glu Asn Arg Ala  
595 600 605

Arg Phe Pro Leu Glu Val Phe Lys Ala Met Arg Ala Met Trp Pro Thr  
610 615 620

Asn Arg Pro Met Ser Val Arg Leu Ser Cys His Asp Trp Phe Pro Gly  
625 630 635 640

Gly Asn Thr Ala Asp Asp Ala Val Ala Ile Ala Arg Leu Phe Lys Glu  
645 650 655

Ala Gly Ala Asp Ile Ile Asp Cys Ser Ser Gly Gln Val Trp Lys Gly  
660 665 670

Asp Gln Pro Val Tyr Gly Arg Met Tyr Gln Thr Pro Phe Ala Asp Arg  
675 680 685

Ile Arg Asn Glu Val Gly Ile Pro Thr Leu Ala Val Gly Ala Ile Ser  
690 695 700

Glu Ala Asp His Ala Asn Ser Ile Ile Ala Ala Gly Arg Ala Asp Leu  
Page 69

705 710 715 720

Cys Ala Ile Ala Arg Pro His Leu Ala Asp Pro Ala Trp Thr Leu His  
725 730 735

Glu Ala Ala Lys Ile Gly Phe Gly Glu Val Ala Trp Pro Lys Gln Tyr  
740 745 750

Arg Ser Ala Arg Gly Gln Tyr Glu Thr Asn Leu Gln Arg Ala Ala Ala  
755 760 765

Ala Val Ala Gly Lys  
770

<210> 90  
<211> 376  
<212> PRT  
<213> Aspergillus fumigatus

<400> 90

Met Arg Glu Glu Pro Ser Ser Ala Gln Leu Phe Lys Pro Leu Lys Val  
1 5 10 15

Gly Arg Cys His Leu Gln His Arg Met Ile Met Ala Pro Thr Thr Arg  
20 25 30

Phe Arg Ala Asp Gly Gln Gly Val Pro Leu Pro Phe Val Gln Glu Tyr  
35 40 45

Tyr Gly Gln Arg Ala Ser Val Pro Gly Thr Leu Leu Ile Thr Glu Ala  
50 55 60

Thr Asp Ile Thr Pro Lys Ala Met Gly Tyr Lys His Val Pro Gly Ile  
65 70 75 80

Trp Ser Glu Pro Gln Arg Glu Ala Trp Arg Glu Ile Val Ser Arg Val  
85 90 95

His Ser Lys Lys Cys Phe Ile Phe Cys Gln Leu Trp Ala Thr Gly Arg  
100 105 110

Ala Ala Asp Pro Asp Val Leu Ala Asp Met Lys Asp Leu Ile Ser Ser  
115 120 125

Ser Ala Val Pro Val Glu Glu Lys Gly Pro Leu Pro Arg Ala Leu Thr  
130 135 140

Glu Asp Glu Ile Gln Gln Cys Ile Ala Asp Phe Ala Gln Ala Ala Arg  
Page 70

P03371US0 Sequence listing).txt

145 150 155 160

Asn Ala Ile Asn Ala Gly Phe Asp Gly Val Glu Ile His Gly Ala Asn  
165 170 175

Gly Tyr Leu Ile Asp Gln Phe Thr Gln Lys Ser Cys Asn His Arg Gln  
180 185 190

Asp Arg Trp Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe Ala Val Glu  
195 200 205

Val Thr Arg Ala Val Ile Glu Ala Val Gly Ala Asp Arg Val Gly Val  
210 215 220

Lys Leu Ser Pro Tyr Ser Gln Tyr Leu Gly Met Gly Thr Met Asp Glu  
225 230 235 240

Leu Val Pro Gln Phe Glu Tyr Leu Ile Ala Gln Met Arg Arg Leu Asp  
245 250 255

Val Ala Tyr Leu His Leu Ala Asn Ser Arg Trp Leu Asp Glu Glu Lys  
260 265 270

Pro His Pro Asp Pro Asn His Glu Val Phe Val Arg Val Trp Gly Gln  
275 280 285

Ser Ser Pro Ile Leu Leu Ala Gly Gly Tyr Asp Ala Ala Ser Ala Glu  
290 295 300

Lys Val Thr Glu Gln Met Ala Ala Ala Thr Tyr Thr Asn Val Ala Ile  
305 310 315 320

Ala Phe Gly Arg Tyr Phe Ile Ser Thr Pro Asp Leu Pro Phe Arg Val  
325 330 335

Met Ala Gly Ile Gln Leu Gln Lys Tyr Asp Arg Ala Ser Phe Tyr Ser  
340 345 350

Thr Leu Ser Arg Glu Gly Tyr Leu Asp Tyr Pro Phe Ser Ala Glu Tyr  
355 360 365

Met Ala Leu His Asn Phe Pro Val  
370 375

<210> 91  
<211> 409  
<212> PRT  
<213> Aspergillus fumigatus

P03371US0 Sequence listing).txt

<400> 91

Met Thr Ile Arg Lys Leu Asp Gly Glu Glu Ser Met Leu Phe Gln Pro  
1 5 10 15

Leu Glu Ile Ala Asn Gly Arg Ile Arg Leu Ser His Arg Val Val His  
20 25 30

Ala Pro Met Thr Arg Asn Arg Gly Val Pro Leu Asn Pro Thr Ser Thr  
35 40 45

Pro Glu Gln Pro Asn Arg Ile Trp Tyr Pro Gly Asp Leu Met Val Gln  
50 55 60

Tyr Tyr Arg Gln Arg Ala Thr Pro Gly Gly Leu Ile Ile Ser Glu Gly  
65 70 75 80

Val Pro Pro Ser Leu Glu Ser Asn Gly Met Pro Gly Val Pro Gly Leu  
85 90 95

Trp Thr Pro Glu Gln Ala Ala Gly Trp Lys Arg Val Val Asp Ala Val  
100 105 110

His Glu Gln Gly Gly Tyr Ile Tyr Cys Gln Leu Trp His Ala Gly Arg  
115 120 125

Ala Thr Ile Pro Gln Met Thr Gly Ser Pro Ala Val Ser Ala Ser Ala  
130 135 140

Thr Val Trp Asp Ser Pro Thr Glu Cys Tyr Ser His Pro Pro Val Gly  
145 150 155 160

Ser Thr Glu Pro Val Arg Tyr Ala Asp His Pro Pro Ile Glu Leu Thr  
165 170 175

Ile Pro His Leu Lys Gln Thr Ile Arg Asp Tyr Cys Asn Ala Ala Lys  
180 185 190

Thr Ala Met Glu Ile Gly Phe Asp Gly Val Glu Leu His Ala Gly Asn  
195 200 205

Gly Tyr Leu Pro Glu Gln Phe Leu Ser Ser Asn Val Asn Lys Arg Thr  
210 215 220

Asp Glu Tyr Gly Gly Ser Pro Glu Lys Arg Cys Arg Phe Val Leu Glu  
225 230 235 240

P03371US0 Sequence listing).txt

Leu Met Asp Glu Leu Ala Ala Thr Val Gly Glu Asp Asn Leu Ala Ile  
245 250 255

Arg Leu Ser Pro Phe Gly Leu Phe Asn Gln Ala Arg Gly Glu Gln Arg  
260 265 270

Val Glu Thr Trp Thr Phe Leu Cys Glu Ser Leu Lys Lys Ala His Pro  
275 280 285

Asn Leu Ser Tyr Val Ser Phe Ile Glu Pro Arg Tyr Glu Gln Ile Phe  
290 295 300

Ser Tyr Glu Glu Lys Asp Asn Phe Leu Arg Ser Trp Gly Leu Ser Asp  
305 310 315 320

Val Asp Leu Ser Ser Phe Arg Lys Ile Phe Gly Thr Thr Pro Phe Phe  
325 330 335

Ser Ala Gly Gly Trp Asp Gln Ser Asn Ser Trp Gly Val Leu Glu Glu  
340 345 350

Gly Arg Tyr Asp Ala Leu Leu Tyr Gly Arg Tyr Phe Thr Ser Asn Pro  
355 360 365

Asp Leu Val Glu Arg Leu Arg Lys Gly Ile Pro Phe Thr Pro Tyr Asp  
370 375 380

Arg Ser Arg Phe Tyr Gly Pro Phe Glu Asp Asn Ala Lys Cys Tyr Val  
385 390 395 400

Asp Tyr Pro Pro Ala Thr Ala Ser Ser  
405

<210> 92  
<211> 406  
<212> PRT  
<213> Candida albicans

<400> 92

Met Thr Val Glu Ser Thr Asn Ser Phe Val Val Pro Ala Gly Thr Lys  
1 5 10 15

Gln Ile Glu Ile Ala Pro Leu Gly Ser Thr Lys Leu Phe Gln Pro Ile  
20 25 30

Lys Val Gly Lys Asn Ile Leu Pro His Arg Val Ala His Ala Pro Thr  
35 40 45

P03371US0 Sequence listing).txt

Thr Arg Phe Arg Ala Ala Lys Asn His Thr Pro Ser Asp Leu Gln Leu  
50 55 60

Glu Tyr Tyr Lys Thr His Ser Gln Tyr Pro Gly Thr Leu Ile Ile Thr  
65 70 75 80

Glu Ala Thr Phe Thr Ser Glu Gln Gly Gly Met Asp Leu His Val Pro  
85 90 95

Gly Ile Tyr Asn Asp Ala Gln Thr Lys Ala Trp Lys Lys Ile Asn Asp  
100 105 110

Glu Ile His Ala Asn Gly Ser Phe Ser Ser Met Gln Leu Trp Tyr Leu  
115 120 125

Gly Arg Val Ala Asn Pro Lys Asp Leu Lys Asp Ala Gly Leu Pro Leu  
130 135 140

Ile Gly Pro Ser Ala Val Tyr Trp Asp Glu Glu Ser Glu Lys Leu Ala  
145 150 155 160

Lys Ser Val Gly Asn Glu Leu Arg Glu Leu Thr Glu Lys Glu Ile Asp  
165 170 175

His Ile Val Glu Val Glu Tyr Pro Asn Ala Ala Lys Arg Ala Ile Glu  
180 185 190

Ala Gly Phe Asp Tyr Ile Glu Val His Ser Ala Pro Gly Tyr Phe Leu  
195 200 205

Asp Gln Phe Leu Asn Pro Ala Ser Asn Lys Arg Thr Asp Lys Tyr Gly  
210 215 220

Gly Ser Ile Glu Asn Arg Ala Arg Leu Leu Leu Arg Ile Ile Asp Lys  
225 230 235 240

Leu Ile Gly Ile Val Gly Ala Glu Lys Leu Ala Val Arg Leu Ala Pro  
245 250 255

Trp Ser Ser Phe Leu Gly Met Glu Ile Glu Gly Glu Glu Ile His Ser  
260 265 270

Tyr Ile Leu Gln Gln Leu Gln Gln Arg Ala Asp Asn Gly Gln Gln Leu  
275 280 285

Ala Tyr Val Ser Leu Ile Glu Pro Arg Val Ile Gly Ile Phe Asp Ala  
290 295 300

P03371U50 Sequence listing).txt

Ser Leu Glu Asp Gln Lys Gly Arg Ser Asn Glu Phe Ala Tyr Lys Tyr  
305 310 315 320

Trp Lys Gly Asn Phe Val Arg Ala Gly Asn Tyr Thr Tyr Asp Ala Pro  
325 330 335

Glu Phe Lys Thr Leu Leu His Asp Leu Asp Asn Asp Arg Thr Ile Val  
340 345 350

Gly Phe Ala Arg Phe Phe Thr Ser Asn Pro Asp Leu Val Glu Lys Leu  
355 360 365

Lys Leu Gly Lys Pro Leu Asn His Tyr Asp Arg Glu Glu Phe Tyr Lys  
370 375 380

Tyr Tyr Asn Tyr Gly Tyr Asn Ser Tyr Asp Glu Ser Glu Lys Gln Val  
385 390 395 400

Ile Gly Lys Pro Leu Val  
405

<210> 93

<211> 406

<212> PRT

<213> Candida albicans

<400> 93

Met Thr Ile Glu Ser Thr Asn Ser Phe Val Val Pro Ser Asp Thr Lys  
1 5 10 15

Leu Ile Asp Val Thr Pro Leu Gly Ser Thr Lys Leu Phe Gln Pro Ile  
20 25 30

Lys Val Gly Asn Asn Val Leu Pro Gln Arg Ile Ala Tyr Val Pro Thr  
35 40 45

Thr Arg Phe Arg Ala Ser Lys Asp His Ile Pro Ser Asp Leu Gln Leu  
50 55 60

Asn Tyr Tyr Asn Ala Arg Ser Gln Tyr Pro Gly Thr Leu Ile Ile Thr  
65 70 75 80

Glu Ala Thr Phe Ala Ser Glu Arg Gly Gly Ile Asp Leu His Val Pro  
85 90 95

Gly Ile Tyr Asn Asp Ala Gln Ala Lys Ser Trp Lys Lys Ile Asn Glu  
100 105 110

P03371U50 Sequence listing).txt

Ala Ile His Gly Asn Gly Ser Phe Ser Ser Val Gln Leu Trp Tyr Leu  
115 120 125

Gly Arg Val Ala Asn Ala Lys Asp Leu Lys Asp Ser Gly Leu Pro Leu  
130 135 140

Ile Ala Pro Ser Ala Val Tyr Trp Asp Glu Asn Ser Glu Lys Leu Ala  
145 150 155 160

Lys Glu Ala Gly Asn Glu Leu Arg Ala Leu Thr Glu Glu Glu Ile Asp  
165 170 175

His Ile Val Glu Val Glu Tyr Pro Asn Ala Ala Lys His Ala Leu Glu  
180 185 190

Ala Gly Phe Asp Tyr Val Glu Ile His Gly Ala His Gly Tyr Leu Leu  
195 200 205

Asp Gln Phe Leu Asn Leu Ala Ser Asn Lys Arg Thr Asp Lys Tyr Gly  
210 215 220

Cys Gly Ser Ile Glu Asn Arg Ala Arg Leu Leu Leu Arg Val Val Asp  
225 230 235 240

Lys Leu Ile Glu Val Val Gly Ala Asn Arg Leu Ala Leu Arg Leu Ser  
245 250 255

Pro Trp Ala Ser Phe Gln Gly Met Glu Ile Glu Gly Glu Glu Ile His  
260 265 270

Ser Tyr Ile Leu Gln Gln Leu Gln Gln Arg Ala Asp Asn Gly Gln Gln  
275 280 285

Leu Ala Tyr Ile Ser Leu Val Glu Pro Arg Val Thr Gly Ile Tyr Asp  
290 295 300

Val Ser Leu Lys Asp Gln Gln Gly Arg Ser Asn Glu Phe Ala Tyr Lys  
305 310 315 320

Ile Trp Lys Gly Asn Phe Ile Arg Ala Gly Asn Tyr Thr Tyr Asp Ala  
325 330 335

Pro Glu Phe Lys Thr Leu Ile Asn Asp Leu Lys Asn Asp Arg Ser Ile  
340 345 350

Ile Gly Phe Ser Arg Phe Phe Thr Ser Asn Pro Asp Leu Val Glu Lys  
355 360 365

P03371US0 Sequence listing).txt

Leu Lys Leu Gly Lys Pro Leu Asn Tyr Tyr Asn Arg Glu Glu Phe Tyr  
370 375 380

Lys Tyr Tyr Asn Tyr Gly Tyr Asn Ser Tyr Asp Glu Ser Glu Lys Gln  
385 390 395 400

Val Ile Gly Lys Pro Leu  
405

<210> 94  
<211> 379  
<212> PRT  
<213> Neurospora crassa

<400> 94

Met Ala Ala Thr Ala Ala Glu Ser Arg Leu Phe Gln Pro Leu Lys Leu  
1 5 10 15

Thr Pro Lys Ile Thr Leu Gly His Arg Leu Ala Met Ala Pro Leu Thr  
20 25 30

Arg Phe Arg Ser Asp Asp Glu His Val Pro Ile Val Pro Leu Met Thr  
35 40 45

Thr Tyr Tyr Ser Gln Arg Ala Ser Val Pro Gly Thr Leu Leu Val Thr  
50 55 60

Glu Ala Thr Phe Ile Ser Pro Ala Ala Gly Gly Tyr Asp Asn Val Pro  
65 70 75 80

Gly Ile Tyr Asn Ala Ala Gln Ile Ala Ala Trp Lys Lys Ile Thr Asp  
85 90 95

Ala Val His Ala Lys Gly Ser Phe Ile Phe Cys Gln Leu Trp Ser Leu  
100 105 110

Gly Arg Ala Ala Asn Pro Glu Val Leu Ala Lys Glu Gly Gly Leu Lys  
115 120 125

Leu Lys Ser Ser Ser Ala Val Pro Met Glu Glu Gly Ala Pro Val Pro  
130 135 140

Glu Glu Met Thr Val Ala Glu Ile Lys Glu Arg Val Ala Glu Tyr Ala  
145 150 155 160

Ala Ala Ala Lys Asn Ala Val Glu Ala Gly Phe Asp Gly Val Glu Ile  
165 170 175

P03371US0 Sequence listing).txt

His Gly Ala Asn Gly Tyr Leu Ile Asp Gln Phe Leu Gln Asp Thr Cys  
180 185 190

Asn Gln Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ser Arg  
195 200 205

Phe Ala His Glu Val Val Lys Ala Val Val Glu Ala Val Gly Ala Glu  
210 215 220

Lys Thr Gly Ile Arg Leu Ser Pro Tyr Ser Thr Phe Gln Gly Met Lys  
225 230 235 240

Met Lys Lys Asp Leu Ile Pro Gln Phe Glu Asp Val Ile Arg Lys Ile  
245 250 255

Asn Gly Phe Gly Leu Ala Tyr Leu His Leu Thr Gln Ser Arg Val Ala  
260 265 270

Gly Asn Met Asp Val Gln Pro Glu Glu Asp Glu Glu Asn Leu Ala Phe  
275 280 285

Ala Ala Lys Leu Trp Asp Gly Pro Leu Leu Ile Ala Gly Gly Leu Thr  
290 295 300

Pro Glu Thr Ala Lys His Leu Val Asp Arg Glu Phe Pro Glu Lys Asp  
305 310 315 320

Val Val Ala Thr Phe Gly Arg His Phe Ile Ser Thr Pro Asp Leu Pro  
325 330 335

Phe Arg Ile Lys Glu Gly Ile Glu Leu Asn Pro Tyr Asp Arg Asp Thr  
340 345 350

Phe Tyr Lys Ala Lys Ser Pro Asp Gly Tyr Ile Asp Gln Pro Phe Ser  
355 360 365

Lys Glu Phe Glu Lys Val Tyr Gly Ala Gln Ala  
370 375

<210> 95  
<211> 400  
<212> PRT  
<213> Saccharomyces cerevisiae  
  
<400> 95

Met Ser Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Gly Asp Thr Asn  
1 5 10 15

P03371US0 Sequence listing).txt

Leu Phe Lys Pro Ile Lys Ile Gly Asn Asn Glu Leu Leu His Arg Ala  
20 25 30

Val Ile Pro Pro Leu Thr Arg Met Arg Ala Leu His Pro Gly Asn Ile  
35 40 45

Pro Asn Arg Asp Trp Ala Val Glu Tyr Tyr Thr Gln Arg Ala Gln Arg  
50 55 60

Pro Gly Thr Met Ile Ile Thr Glu Gly Ala Phe Ile Ser Pro Gln Ala  
65 70 75 80

Gly Gly Tyr Asp Asn Ala Pro Gly Val Trp Ser Glu Glu Gln Met Val  
85 90 95

Glu Trp Thr Lys Ile Phe Asn Ala Ile His Glu Lys Lys Ser Phe Val  
100 105 110

Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Asn Leu  
115 120 125

Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Phe Met  
130 135 140

Asp Ala Glu Gln Glu Ala Lys Ala Lys Lys Ala Asn Asn Pro Gln His  
145 150 155 160

Ser Leu Thr Lys Asp Glu Ile Lys Gln Tyr Ile Lys Glu Tyr Val Gln  
165 170 175

Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His  
180 185 190

Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn  
195 200 205

Thr Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe  
210 215 220

Thr Leu Glu Val Val Asp Ala Leu Val Glu Ala Ile Gly His Glu Lys  
225 230 235 240

Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly  
245 250 255

Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Ala Gly Glu

P03371US0 Sequence listing).txt

260

265

270

Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu  
275 280 285

Val Glu Pro Arg Val Thr Asn Pro Phe Leu Thr Glu Gly Glu Gly Glu  
290 295 300

Tyr Glu Gly Gly Ser Asn Asp Phe Val Tyr Ser Ile Trp Lys Gly Pro  
305 310 315 320

Val Ile Arg Ala Gly Asn Phe Ala Leu His Pro Glu Val Val Arg Glu  
325 330 335

Glu Val Lys Asp Lys Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile  
340 345 350

Ser Asn Pro Asp Leu Val Asp Arg Leu Glu Lys Gly Leu Pro Leu Asn  
355 360 365

Lys Tyr Asp Arg Asp Thr Phe Tyr Gln Met Ser Ala His Gly Tyr Ile  
370 375 380

Asp Tyr Pro Thr Tyr Glu Glu Ala Leu Lys Leu Gly Trp Asp Lys Lys  
385 390 395 400

<210> 96  
<211> 400  
<212> PRT  
<213> Saccharomyces cerevisiae  
<400> 96

Met Pro Phe Val Lys Asp Phe Lys Pro Gln Ala Leu Gly Asp Thr Asn  
1 5 10 15

Leu Phe Lys Pro Ile Lys Ile Gly Asn Asn Glu Leu Leu His Arg Ala  
20 25 30

Val Ile Pro Pro Leu Thr Arg Met Arg Ala Gln His Pro Gly Asn Ile  
35 40 45

Pro Asn Arg Asp Trp Ala Val Glu Tyr Tyr Ala Gln Arg Ala Gln Arg  
50 55 60

Pro Gly Thr Leu Ile Ile Thr Glu Gly Thr Phe Pro Ser Pro Gln Ser  
65 70 75 80

Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Glu Glu Gln Ile Lys  
Page 80

Glu Trp Thr Lys Ile Phe Lys Ala Ile His Glu Asn Lys Ser Phe Ala  
100 105 110

Trp Val Gln Leu Trp Val Leu Gly Trp Ala Ala Phe Pro Asp Thr Leu  
115 120 125

Ala Arg Asp Gly Leu Arg Tyr Asp Ser Ala Ser Asp Asn Val Tyr Met  
130 135 140

Asn Ala Glu Gln Glu Glu Lys Ala Lys Lys Ala Asn Asn Pro Gln His  
145 150 155 160

Ser Ile Thr Lys Asp Glu Ile Lys Gln Tyr Val Lys Glu Tyr Val Gln  
165 170 175

Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His  
180 185 190

Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn  
195 200 205

Asn Arg Thr Asp Glu Tyr Gly Gly Ser Ile Glu Asn Arg Ala Arg Phe  
210 215 220

Thr Leu Glu Val Val Asp Ala Val Val Asp Ala Ile Gly Pro Glu Lys  
225 230 235 240

Val Gly Leu Arg Leu Ser Pro Tyr Gly Val Phe Asn Ser Met Ser Gly  
245 250 255

Gly Ala Glu Thr Gly Ile Val Ala Gln Tyr Ala Tyr Val Leu Gly Glu  
260 265 270

Leu Glu Arg Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu  
275 280 285

Val Glu Pro Arg Val Thr Asn Pro Phe Leu Thr Glu Gly Glu Gly Glu  
290 295 300

Tyr Asn Gly Gly Ser Asn Lys Phe Ala Tyr Ser Ile Trp Lys Gly Pro  
305 310 315 320

Ile Ile Arg Ala Gly Asn Phe Ala Leu His Pro Glu Val Val Arg Glu  
325 330 335

P03371US0 Sequence listing).txt

Glu Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile  
340 345 350

Ser Asn Pro Asp Leu Val Asp Arg Leu Glu Lys Gly Leu Pro Leu Asn  
355 360 365

Lys Tyr Asp Arg Asp Thr Phe Tyr Lys Met Ser Ala Glu Gly Tyr Ile  
370 375 380

Asp Tyr Pro Thr Tyr Glu Glu Ala Leu Lys Leu Gly Trp Asp Lys Asn  
385 390 395 400

<210> 97

<211> 400

<212> PRT

<213> Saccharomyces cerevisiae

<400> 97

Met Pro Phe Val Lys Gly Phe Glu Pro Ile Ser Leu Arg Asp Thr Asn  
1 5 10 15

Leu Phe Glu Pro Ile Lys Ile Gly Asn Thr Gln Leu Ala His Arg Ala  
20 25 30

Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile  
35 40 45

Pro Asn Lys Glu Trp Ala Ala Val Tyr Tyr Gly Gln Arg Ala Gln Arg  
50 55 60

Pro Gly Thr Met Ile Ile Thr Glu Gly Thr Phe Ile Ser Pro Gln Ala  
65 70 75 80

Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Asp Glu Gln Val Ala  
85 90 95

Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala  
100 105 110

Trp Val Gln Leu Trp Ser Leu Gly Trp Ala Ser Phe Pro Asp Val Leu  
115 120 125

Ala Arg Asp Gly Leu Arg Tyr Asp Cys Ala Ser Asp Arg Val Tyr Met  
130 135 140

Asn Ala Thr Leu Gln Glu Lys Ala Lys Asp Ala Asn Asn Leu Glu His  
145 150 155 160

P03371US0 Sequence listing).txt

Ser Leu Thr Lys Asp Asp Ile Lys Gln Tyr Ile Lys Asp Tyr Ile His  
165 170 175

Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His  
180 185 190

Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn  
195 200 205

Lys Arg Thr Asp Glu Tyr Gly Gly Thr Ile Glu Asn Arg Ala Arg Phe  
210 215 220

Thr Leu Glu Val Val Asp Ala Leu Ile Glu Thr Ile Gly Pro Glu Arg  
225 230 235 240

Val Gly Leu Arg Leu Ser Pro Tyr Gly Thr Phe Asn Ser Met Ser Gly  
245 250 255

Gly Ala Glu Pro Gly Ile Ile Ala Gln Tyr Ser Tyr Val Leu Gly Glu  
260 265 270

Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu  
275 280 285

Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu  
290 295 300

Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro  
305 310 315 320

Ile Ile Arg Ala Gly Asn Tyr Ala Leu His Pro Glu Val Val Arg Glu  
325 330 335

Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile  
340 345 350

Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn  
355 360 365

Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr  
370 375 380

Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn  
385 390 395 400

<210> 98  
<211> 26  
<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 98

gctagcatga ctgtcgccga tatcga

26

<210> 99

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 99

gctagcctat acatcgaaaa tagactgc

28

<210> 100

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 100

actagtccag gggactgtcg tgggtcaa

27

<210> 101

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 101

caattgccca ggcctaatagc atgctg

26